



BEST AVAILABLE COPY

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10	20	30	40	50	60
MALAGAPAG	PCAPALEALL	GAGALRLDS	SQIVIISAAQ	DASAPPAPTG	PAAPAAAGPCD
70	80	90	100	110	120
POLLLEFATPQ	APRPTPSAPR	PALGRPPVKR	RDLLETDHQY	LAESSGPARG	RGRHPGKGVK
130	140	150	160	170	180
SPGEKSRYET	SLNLTTKREL	ELLSHSADGV	VDLNWAAEVL	KVQKRRIYDI	TNVLEGIQLI
190	200	210	220	230	240
AKKSKNHIQW	LGSHTTWGVG	GRLEGLTQDL	RQLQESEQQL	DHLMNICTTQ	LRLLEDTS
250	260	270	280	290	300
QRLAYVTCQD	LRSIADPAEQ	MVMVIKAPPE	TQLQAVDSSE	NEQISLKSQ	GPIDVFLCPE
310	320	330	340	350	360
ETVGGISPGK	TPSQEVTSEE	ENRATDSATI	VSPPPSSPPS	SLTTDPSQSL	LSLEQEPLLS
370	380	390	400	410	420
RMGSLRAPVD	EDRLSPLVAA	DSLLEHVRED	FSGLLPEEFI	SLSPPHEALD	YHFGLEEGER
430	440	450	460	470	480
IRDLFDCDEG	DLTPLDF*

FIG 1A.



10 GGAATTCCGT 20 GGCCGGGACT 30 TTGCAGGCAG 40 CCGCGGCCCG 50 GGGCGGAGCG 60 GGATCGAGCC
70 CTCGCCGAGG 80 CCTGCCGCCA 90 TGGGCCCGCG 100 CCGCCGCCCG 110 CGCCTGTCAC 120 CCGGGCCGCG
130 CCGGCCGTGA 140 GCGTCATGCG 150 CTTGGCCCGG 160 GCCCCCTGCG 170 GCGGCCCATG 180 CCGGCCGCGG
190 CTGGAGGCC 200 TGCTCGGGCG 210 CCGCGCGCTG 220 CCGCTGCTCG 230 ACTCCTCGCA 240 GATCGTCATC
250 ATCTCCGCCG 260 CGCAGGACGC 270 CAGCGCCCCG 280 CCGGCTCCCA 290 CCGGCCCCCG 300 GCGGCCCGCC
310 GCCGGCCCCCT 320 GCGACCCCTGA 330 CCTGCTGCTC 340 TTCGCCACAC 350 CGCAGGCGCC 360 CCGGCCCA
370 CCCAGTGCGC 380 CGCGGCCCGC 390 GCTCGGCCCG 400 CCGCCGGTGA 410 AGCGGAGGCT 420 GGACCTGGAA
430 ACTGACCATC 440 AGTACCTGGC 450 CGAGAGCAGT 460 GGGCCAGCTC 470 GGGCAGAGG 480 CCGCCATCCA
490 GGAAAAGGTG 500 TGAAATCCCC 510 GGGGAGAAAG 520 TCACGCTATG 530 AGACCTCACT 540 GAATCTGACC
550 ACCAAGCGCT 560 TCCTGGAGCT 570 GCTGAGCCAC 580 TCGGCTGACG 590 GTGTCGTCGA 600 CCTGAAGTGG
610 GCTGCCGAGG 620 TGCTGAAGGT 630 GCAGAAAGCG 640 CGCATCTATG 650 ACATCACCAA 660 CGTCCTTGAG

FIG 1B-1.

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670	680	690	700	710	720
GGCATCCAGC	TCATTGCCAA	GAAGTCCAAG	AACCACATCC	AGTGGCTGGG	CAGCCACACC
730	740	750	760	770	780
ACAGTGGGCG	TCGGCGGACG	GCTTGAGGGG	TTGACCCAGG	ACCTCCGACA	GCTGCAGGAG
790	800	810	820	830	840
AGCGAGCAGC	AGCTGGACCA	CCTGATGAAT	ATCTGTACTA	CGCAGCTGCG	CCTGCTCTCC
850	860	870	880	890	900
GAGGACACTG	ACAGCCAGCG	CCTGGCCTAC	GTGACGTGTC	AGGACCTTCG	TAGCATTTGCA
910	920	930	940	950	960
GACCCCTGCAG	AGCAGATGGT	TATGGTGATC	AAAGCCCCCTC	CTGAGACCCA	GCTCCAAGCC
970	980	990	1000	1010	1020
GTGGACTCTT	CGGAGAACTT	TCAGATCTCC	CTTAAGAGCA	AACAAGGCCC	GATCGATGTT
1030	1040	1050	1060	1070	1080
TTCCTGTGCC	CTGAGGAGAC	CGTAGGTGGG	ATCAGCCCTG	GGAAGACCCC	ATCCCAGGAG
1090	1100	1110	1120	1130	1140
GTCACCTTCTG	AGGAGGAGAA	CAGGGCCACT	GACTCTGCCA	CCATAGTGTC	ACCACCACCA
1150	1160	1170	1180	1190	1200
TCATCTCCCC	CCTCATCCCT	CACCACAGAT	CCCAGCCAGT	CTCTACTCAG	CCTGGAGCAA
1210	1220	1230	1240	1250	1260
GAACCGCTGT	TGTCCCGGAT	GGCAGCCCTG	CGGGCTCCCG	TGGACGAGGA	CCGCCTGTCC

FIG. 1B-2.

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1270	1280	1290	1300	1310	1320
CCGCTGGTGG	CGCCGACTC	GCTCCTGGAG	CATGTGCGGG	AGGACTTCTC	CGGCTCCTC
1330	1340	1350	1360	1370	1380
CCTGAGGAGT	TCATCAGCCT	TTCCCCACCC	CACGAGGCC	TCGACTACCA	CTTCGGCCTC
1390	1400	1410	1420	1430	1440
GAGGAGGGCG	AGGGCATCAG	AGACCTCTTC	GACTGTGACT	TTGGGGACCT	CACCCCCCTG
1450	1460	1470	1480	1490	1500
GATTCTGAC	AGGGCTTGA	GGGACCAGGG	TTTCCAGAGT	AGCTCACCTT	GTCTCTGCAG
1510	1520	1530	1540	1550	1560
CCCTGGAGCC	CCCTGTCCCT	GGCCGTCCCTC	CCAGCCCTGTT	TGGAACATT	TAATTATAC
1570	1580	1590	1600	1610	1620
CCCTCTCCTC	TGTCTCCAGA	AGCTTCTAGC	TCTGGGGTCT	GGCTACCGCT	AGGAGGCTGA
1630	1640	1650	1660	1670	1680
GCAAGCCAGG	AAGGGAAGGA	GTCTGTGTGG	TGTGTATGTG	CATGCAGCCT	ACACCCACAC
1690	1700	1710	1720	1730	1740
GTGTGTACCG	GGGTGAATG	TGTGTGAGCA	TGTGTGTGTG	CATGTACCGG	GGAATGAAGG
1750	1760	1770	1780	1790	1800
TGAACATACA	CCTCTGTGTG	TGCACTGCAG	ACACGCCCCA	GTGTGTCCAC	ATGTGTGTGC
1810	1820	1830	1840	1850	1860
ATGAGTCCAT	CTCTGCCCGT	GGGGGGGCTC	TAACTGCACT	TTCCGGCCCTT	TTGCTCGTGG
1870	1880	1890	1900	1910	1920
GGTCCCACAA	GGCCCAGGGC	AGTGCCCTGCT	CCCAGAAATCT	GGTGCTCTGA	CCAGGCCCAGG

FIG. 1B-3.

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1930	1940	1950	1960	1970	1980
TGGGGAGGCT	TTGGCTGGCT	GGGCGTGTA	GACGGTGAGA	GCACTTCTGT	CTTAAAGGTT
1990	2000	2010	2020	2030	2040
TTTTCTGATT	GAAGCTTTAA	TGGAGCGTTA	TTTATTTATC	GAGGCCCTCTT	TGGTGAGCCT
2050	2060	2070	2080	2090	2100
GGGGAATCAG	CAAAAGGGA	GGAGGGGTGT	GGGGTTGATA	CCCCAACTCC	CTCTACCCCTT
2110	2120	2130	2140	2150	2160
GAGCAAGGCG	AGGGGTCCCT	GAGCTGTTCT	TCTGCCCCAT	ACTGAAGGAA	CTGAGGCCCTG
2170	2180	2190	2200	2210	2220
GGTGATTAT	TTATTGGGAA	AGTGAGGGAG	GGAGACAGAC	TGACTGACAG	CCATGGGTGG
2230	2240	2250	2260	2270	2280
TCAGATGGTG	GGGTGGGCCC	TCTCCAGGGG	GCCAGTTCAG	GGCCCAGCTG	CCCCCCAGGA
2290	2300	2310	2320	2330	2340
TGGATATGAG	ATGGGAGAGG	TGAGTGGGGG	ACCTTCACTG	ATGTGGGCAG	GAGGGGTGGT
2350	2360	2370	2380	2390	2400
GAAGGCCCTCC	CCCAGCCCCAG	ACCCTGTGGT	CCCTCCTGCA	GTGTCTGAAG	CGCCTGCCCTC
2410	2420	2430	2440	2450	2460
CCCACCTGCTC	TGCCCCACCC	TCCAATCTGC	ACTTTGATTT	GCTTCCTAAC	AGCTCTGTTC
2470	2480	2490	2500	2520	2520
CCTCCTGCTT	TGGTTTTAAT	AAATATTTTG	ATGACGTTAA	AAAAAGGAAT	TCGATAT

FIG. 1B-4.

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1 ttccgggtttt tctcagggga cgttgaaatt attttgttaa cgggagtcgg gagaggacgg
61 ggcggtgcccc gcgtgcgcgc gcgtcgtcct ccccggcgct cctccacagc tgcgtggctc
121 ccgccgcgga aaggcgtcat gccgcccaa gccgccccc acccccgaa aaacggccgc caccgccgcc
181 gctgccgccg cggaccccc gccgccccc ctcaggcttg gtcaggcttg agtttgaaga acagaaagaa
241 caggacagcg gcccgaggga cctgcctctc tcagaaatta ttcatctgtg gatggagtat atcatgtcag agagagagct
301 cctgatttta ctgcattatg gggagaaagt ttcatctgtg ctgtatcttt attgcagcag ttgacctaga tattcaaaag
361 tgggttaactt gggagaaagt ttcatctgtg ctgtatcttt attgcagcag ttgacctaga ttgacatgtcg
421 aaaaagggaac tgtggggaat ctgtatcttt gaaaaacata gaaatcagtg gataatgcta tgtcaagact gttgaagaag
481 ttcactttta ctgagctaca gaaaaacata taccaaagtt cttcagcaa atctactgaa ataatcttg cattggtgct aaaagtctct
541 ctaaaagaaa ttgataccag tgtttgcact atctactgaa ataatcttg cattggtgct tggaaagatga tctggtgatt
601 tatgatgtat tgtttgcact cttcagcaa atctactgaa ataatcttg cattggtgct tggaaagatga tctggtgatt
661 acacaaccca gcagtttcgat ttttattagc tgtccttgac ttttatta cccattaatg gttcacctcg aacacccagg
721 tggatcacat ttttattagc tgtccttgac ttttatta cccattaatg gttcacctcg aacacccagg aagaattatt
781 tcatttcagt taatgctatg agctgttata acggatagca aacaaactag aagaattatt tgaataatgt ttatttcaaa
841 ctcaagaac cataaaaaac agctgttata acggatagca aacaaactag aagaattatt tgaataatgt ttatttcaaa
901 cgaggtcaga acaggagtg acggatagca aacaaactag aagaattatt tgaataatgt ttatttcaaa
961 gaagttctct gtaagaaca ttctcttga cgaagaaatt tctcttga actgattcta tagacagttt acacactcca
1021 aattttatata cttttatgaa ttctcttga cgaagaaatt tctcttga actgattcta tagacagttt acacactcca
1081 gaaaatcttt cttaacgata aactcttcag ccttgatgaa gaggtgaatg ttaattatga ttttaaatc agcaagtgat
1141 ttatttttgg atcatgataa aactcttcag ccttgatgaa gaggtgaatg ttaattatga ttttaaatc agcaagtgat
1201 agaacaccac gaaaagtaa ccttgatgaa gaggtgaatg ttaattatga ttttaaatc agcaagtgat
1261 gttaggactg ttatgaacac tatccaaca ttcctatctt aacaactgca cagtgaatcc aaaagaaagt
1321 caaccttcag aaaatctgat ttcctatctt aacaactgca cagtgaatcc aaaagaaagt taaagctgtg
1381 atactgaaa gagtgaagga tataggatac atctttaaag agaaatttgc taaagctgtg
1441 ggacagggtt gtgtcgaaat tggatcacag cgatacaaac ttggagttcg cttgtattac

FIG. 2A-1.





1501 cgagtaatgg aatccatgct taaaccagaa gaagaacgat tatccattca aaattttagc
1561 aaacttctga atgacaacat ttttcatatg tctttattgg tctgcgctct tgaggttgta
1621 atggccacat atagcagaag tacatctcag aatcttgatt aatcttgatt ctggaacaga tttgtctttc
1681 ccatggattc tgaatgtgct taatttaaaa gcctttgatt gcctttgatt ttacaaagt gatcgaaagt
1741 ttatcaaag cagaaggcaa ttgacaaga gaaatgataa aacatttaga acgatgtgaa
1801 catcgaatca tggatccct accaactgat cagattcac cttatttga tcttatataa
1861 caatcaaagg accgagaagg tgcagcagat caccttgaat ctgcttgctc ctttaattctt
1921 cctctccaga ataatacac ccaactacgg tgtaaatctt atgtattctt ctctgtaag atctccaaag
1981 aaaaaagggt caactacgg tgtaaatctt actgcaaatg cagagacaca cactgtttta taaaaaagt
2041 gccttccaga ccagaagg cctatctcgg gctaaataca ctttgtgaac ccttctctgc tgcagaatga
2101 tatcggctag cctatctcgg gctaaataca ctttgtgaac ccttctctgc tgcagaatga
2161 gaattagaac atatcatctg gcaattatg ccaaatcatt gtaacagcat acaaggatct tctcatgct
2221 atgagagaca ggcatcttga ccaaatcatt gtaacagcat acaaggatct tctcatgct
2281 aagaatatag accttaaat cattcaaacg cgtcttctat gcagagactg aaacaataa ttttgcagta
2341 gttcaggaga cattcaaacg cgtcttctat gcagagactg aaacaataa ttttgcagta
2401 ttctataact cgtcttctat gcagagactg aaacaataa ttttgcagta ttttgcagta
2461 agggccctta ccttgctcacc aatacctcac agggaaacatc accaacaataa ttttgcagta
2521 tcacccttac ggattcctgg gtctgccaac ttctgagaag aagtgtgaa ggaagcaacc
2581 atttcagaag gtctgccaac ttctgagaag aagtgtgaa ggaagcaacc ggaagcaacc
2641 attggtgaat cattcgggac ttctgagaag aagtgtgaa ggaagcaacc ggaagcaacc
2701 agcgaccgtg tgctcaaaa atattgaagg atcagatgaa gcagatggaa gtaaacatct
2761 ctacgctttg atattgaagg atcagatgaa gcagatggaa gtaaacatct gtaaacatct
2821 tccaaatttc agcagaaact ggcagaaatg acttctactc gaacacgaat gaacacgaat
2881 aaaatgaatg atagcatgga tacctcaaac aaggaagaga aatgaggatc aatgaggatc
2941 ggtggacact gtgtacacct gtgtacacct tgtctctcac agatgtgact agatgtgact

FIG 2A-2.



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"MPPKTPRKTAATAAAAEPPAPPPPPPEEDPEQSGPEDLPL
VRLEFEETEEPDTALCQKLKIPDHVRERAWLTWEKVSSVDGVLGGYIQKKELWGIC
IFIAAVDLDEMSFTTELQKNIEISVHKFFNLLKEIDTSTKVDNAMSRLKKYDVLFA
LFSKLERTECELIYLTQPSSSISTEINSALVLKVSWITFLAKGEVLQMEDDLVISFQL
MLCVLDYFIKLSPPMLLKEPYKTAVIPINGSPLGLVTSNGLPEVENLSKRYEEIYLNKNDLDAR
LCKEHECNIDEVKNVYFKNFIPFMNSLGLVTSNGLPEVENLSKRYEEIYLNKNDLDAR
LFLDHDKTLQTDSIDSFETQRTPRKSNLDEEVNIPPHTPVRTVMNTIQQLMMILNSA
SDQPSENLISYFNNTVNPKESILKRVKDIGYIFKEKFAKAVGQGCVEIGSQRYKLG
RLYVRVMESMLKSEERLSIQNFSKLLNDNIFHMSLLACALEVMATYSRSTSQNLDS
GTDLSFPWILNLKAFDFYKVIESFIKAEGNLTREMIKHLERCHEHRIMESLAWLSD
SPLFDLIKQSKDREGPTDHLLESACPLNPLQNNHTAADMVLSPVRSPPKKKGSTTRVNS
TANAETQATSAFQTQKPLKSTSLFYKKVYRLAYLRLNLTLCERLLSEHPELEHI IWT
LFQHTLQNEYELMRDRHLDQIMMCSMYGICKVKKNIDLKFKIIVTAYKDLPHAVQETFK
RVLIKEEYDSII VFYNSVFMQRLKTNILQYASTRPPTLSPIPHIPRSPYKFPSSPLR
IPGGNIYISPLKSPYKISEGLPTPTKMTPRSRILVSI GESEGTSEKFKINQMVCNSD
RVLKRSAEGSNPPKPLKLRFRDIEGSDEADGSKHLPGESKFKQQLAEMTSTRTRMQKQ
KMND SMDTSNKEEK"

FIG 2B.

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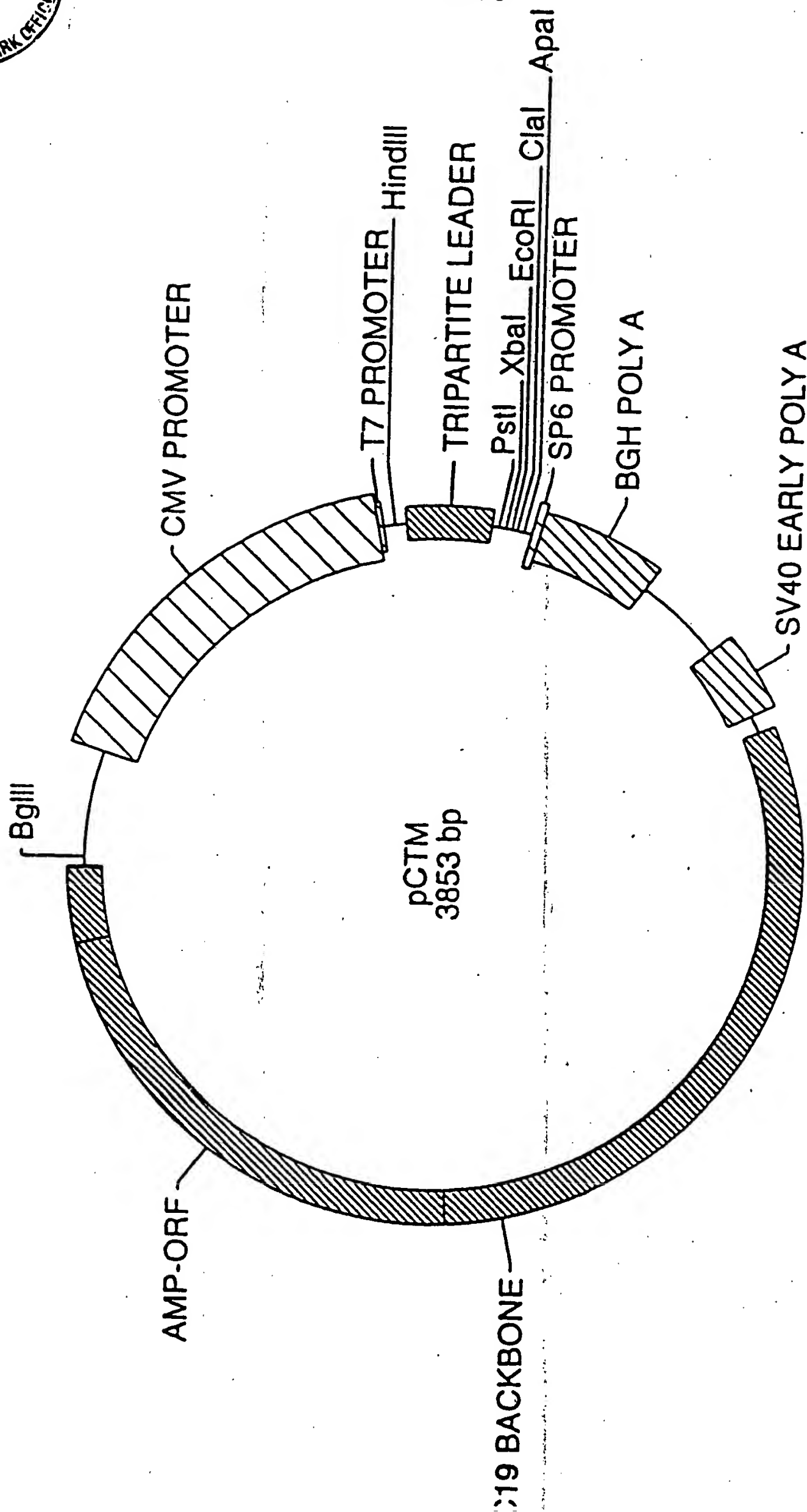


FIG. 3.

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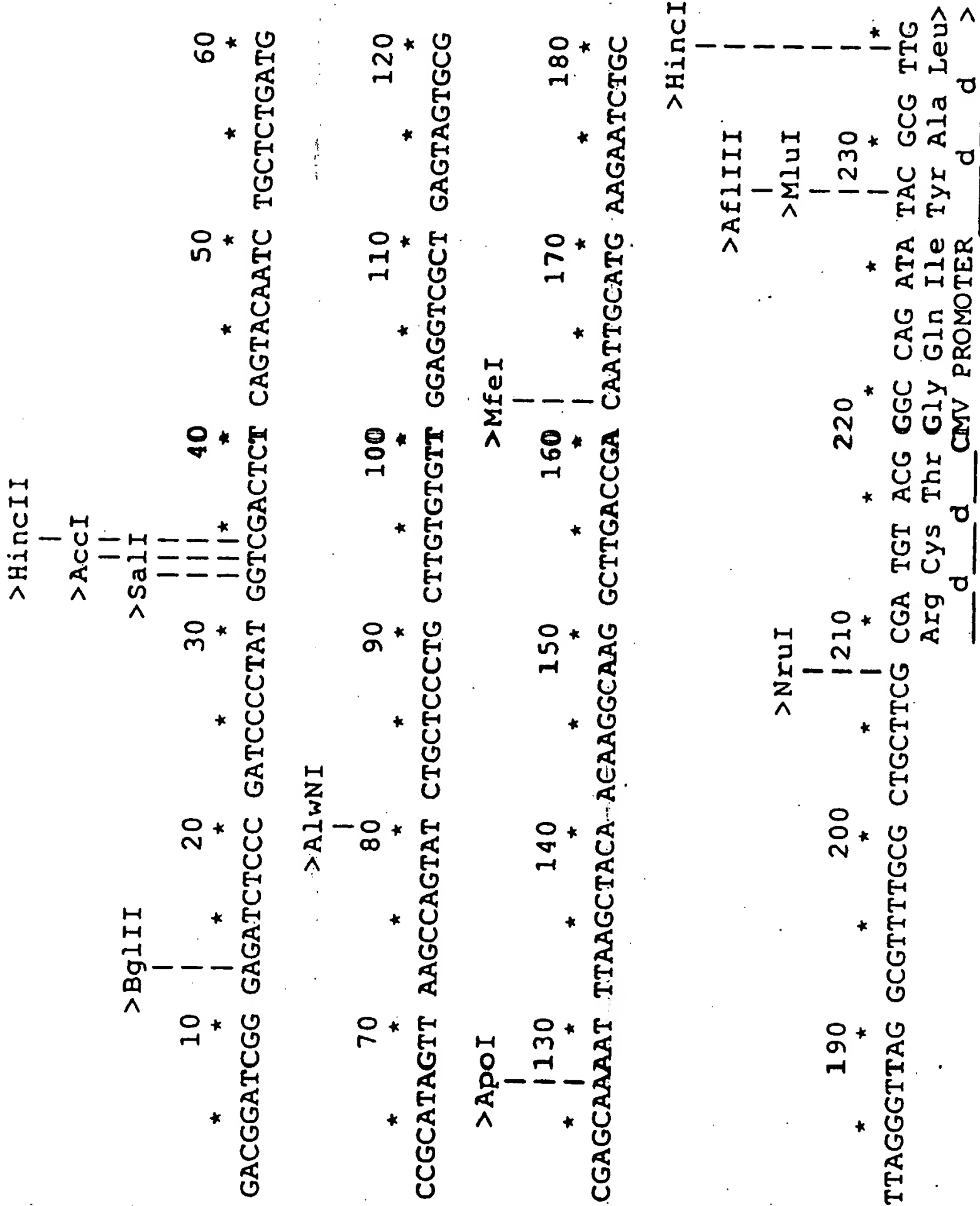


FIG 4-1.

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```
>SpeI      >AseI
|           |
240 *      250 *      260 *      270 *      280 *
ACA TTG ATT ATT GAC TAG TTA ATA GTA ATC AAT TAC GGG GTC ATT
Thr Leu Ile Ile Asp *** Leu Leu Ile Val Ile Asn Tyr Gly Val Ile>
d d d d d CMV PROMOTER d d d d d >

290 *      300 *      310 *      320 *      330 *
AGT TCA TAG CCC ATA TAT GGA GTT CCG CGT TAC ATA ACT TAC GGT AAA
Ser Ser *** Pro Ile Tyr Gly Val Pro Arg Tyr Ile Thr Tyr Gly Lys>
d d d d d CMV PROMOTER d d d d d >

>BglI      >AatII
|           |
340 *      350 *      360 *      370 *
TGG CCC GCC TGG CTG ACC GCC CAA CGA CCC CCG CCC ATT GAC GTC AAT
TTP Pro Ala TTP Leu Thr Ala Gln Arg Pro Pro Pro Ile Asp Val Asn>
d d d d d CMV PROMOTER d d d d d >

380 *      390 *      400 *      410 *      420 *
AAT GAC GTA TGT TCC CAT AGT AAC GCC AAT AGG GAC TTT CCA TTG ACG
Asn Asp Val Cys Ser His Ser Asn Ala Asn Arg Asp Phe Pro Leu Thr>
d d d d d CMV PROMOTER d d d d d >
```

FIG. 4-2.

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```
>AatII
|
430 *
| *
TCA ATG GGT GGA CTA TTT ACG GTA AAC TGC CCA CTT GGC AGT ACA TCA
Ser Met Gly Gly Leu Phe Thr Val Asn Cys Pro Leu Gly Ser Thr Ser>
d d d d d CMV PROMOTER d d d d d >

>BglI
|
460 *
| *
470 *
| *
TCA ATG GGT GGA CTA TTT ACG GTA AAC TGC CCA CTT GGC AGT ACA TCA
Ser Met Gly Gly Leu Phe Thr Val Asn Cys Pro Leu Gly Ser Thr Ser>
d d d d d CMV PROMOTER d d d d d >

>NdeI
|
480 *
| *
| *
AGT GTA TCA TAT GCC AAG TAC GCC CCC TAT TGA CGT CAA TGA CGG TAA
Ser Val Ser Tyr Ala Lys Tyr Ala Pro Tyr *** Arg Gln *** Arg ***>
d d d d d CMV PROMOTER d d d d d >

>BglI
|
530 *
| *
| *
ATG GCC CGC CTG GCA TTA TGC CCA GTA CAT GAC CTT ATG GGA CTT TCC
Met Ala Arg Leu Ala Leu Cys Pro Val His Asp Leu Met Gly Leu Ser>
d d d d d CMV PROMOTER d d d d d >

>NcoI
|
560 *
| *
570 *
| *
TAC TTG GCA GTA CAT CTA CGT ATT AGT CAT CGC TAT TAC CAT GGT GAT
Tyr Leu Ala Val His Leu Arg Ile Ser His Arg Tyr Tyr His Gly Asp>
d d d d d CMV PROMOTER d d d d d >

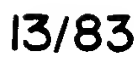
>BsaAI
|
580 *
| *
590 *
| *
600 *
| *
610 *
| *
TAC TTG GCA GTA CAT CTA CGT ATT AGT CAT CGC TAT TAC CAT GGT GAT
Tyr Leu Ala Val His Leu Arg Ile Ser His Arg Tyr Tyr His Gly Asp>
d d d d d CMV PROMOTER d d d d d >

>SnaBI
|
590 *
| *
600 *
| *
610 *
| *
TAC TTG GCA GTA CAT CTA CGT ATT AGT CAT CGC TAT TAC CAT GGT GAT
Tyr Leu Ala Val His Leu Arg Ile Ser His Arg Tyr Tyr His Gly Asp>
d d d d d CMV PROMOTER d d d d d >

>StyI
|
610 *
| *
620 *
| *
TAC TTG GCA GTA CAT CTA CGT ATT AGT CAT CGC TAT TAC CAT GGT GAT
Tyr Leu Ala Val His Leu Arg Ile Ser His Arg Tyr Tyr His Gly Asp>
d d d d d CMV PROMOTER d d d d d >
```

FIG 4-3.

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[illegible]

	720	730	740	750	760
GCA	* CCA AAA TCA ACG GGA CTT TCC AAA ATG TCG TAA CAA CTC CGC CCC	*	*	*	*
Ala	Pro Lys Ser Thr Gly Leu Ser Lys Met Ser *** Gln Leu Arg Pro>				
d	d d d d d CMV PROMOTER d d d d d -d ->				

[illegible]

FIG. 4-4.

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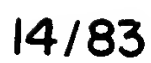


FIG. 4-5.

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>BanII
|
>BsiHKA I
|
>SacI
|
>Ecl136II | >BclI

[illegible]

FIG. 4-7.



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>Bani
|
1210 * 1220 * 1230 * 1240 * 1250 * 1260 *
* * * * *
GTTGTTGCC CCTCCCCCGT GCCTTCCTTG ACCCTGGAAG GTGCCACTCC CACTGTCTCTT
1270 * 1280 * 1290 * 1300 * 1310 * 1320 *
* * * * *
TCCTAATAAA ATGAGGAAAT TGCATCGCAT TGTCTGAGTA GGTGTCATTC TATTCTGGGG

>BbsI
|
1330 * 1340 * 1350 * 1360 * 1370 * 1380 *
* * * * *
GGTGGGGTGG GGCAGGACAG CAAGGGGAG GATTGGGAAG ACAATAGCCG AAATGACCGA

>BssSI
|
>BspMI
|
1390 * 1400 * 1410 * 1420 * 1430 * 1440 *
* * * * *
CCAAGCGACG CCCAACCTGC CATCACGAGA TTTCGATTCC ACCGCCGCCT TCTATGAAAG

>NaeI
|
>BsrFI
|
>BpmI
|
>NgOMI
|
1450 * 1460 * 1470 * 1480 * 1490 * 1500 *
* * * * *
GTTGGGCTTC GGAATCGTTT TCCGGGACGC CGGCTGGATG ATCCTCCAGC GCGGGGATCT

G.4-8.

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```
>BpmI
|
>SV40_early_poly_A
|
1510 * 1520 * 1530 * 1540 * 1550 * 1560 *
CATGCTGGAG TTCTTCGCCC ACCCCAACCTT GTTTATTGCA GCTTATAATG GTTACAAATA

>ApoI
|
1570 * 1580 * 1590 * 1600 * 1610 * 1620 *
AAGCAATAGC ATCACAATTC TCACAAATAA AGCATTTTTC TCACTGCATT CTAGTTGTGG

>HincII
|
>Bst1107I >AccI
|
>AccI >SalI
|
1630 * 1640 * 1650 * 1660 * 1670 * 1680 *
TTTGTCCAAA CTCATCAATG TATCTTATCA TGCTGTATA CCGTCGACCT CTAGCTAGAG

>BsrBI
|
1690 * 1700 * 1710 * 1720 * 1730 * 1740 *
CTTGGCGTAA TCATGGTCAT AGCTGTTCC TGTGTGAAAT TGTATCCGC TCACAATTCC
c PUC19 BACKBONE H3 TO AATII c
```

FIG 4-9.

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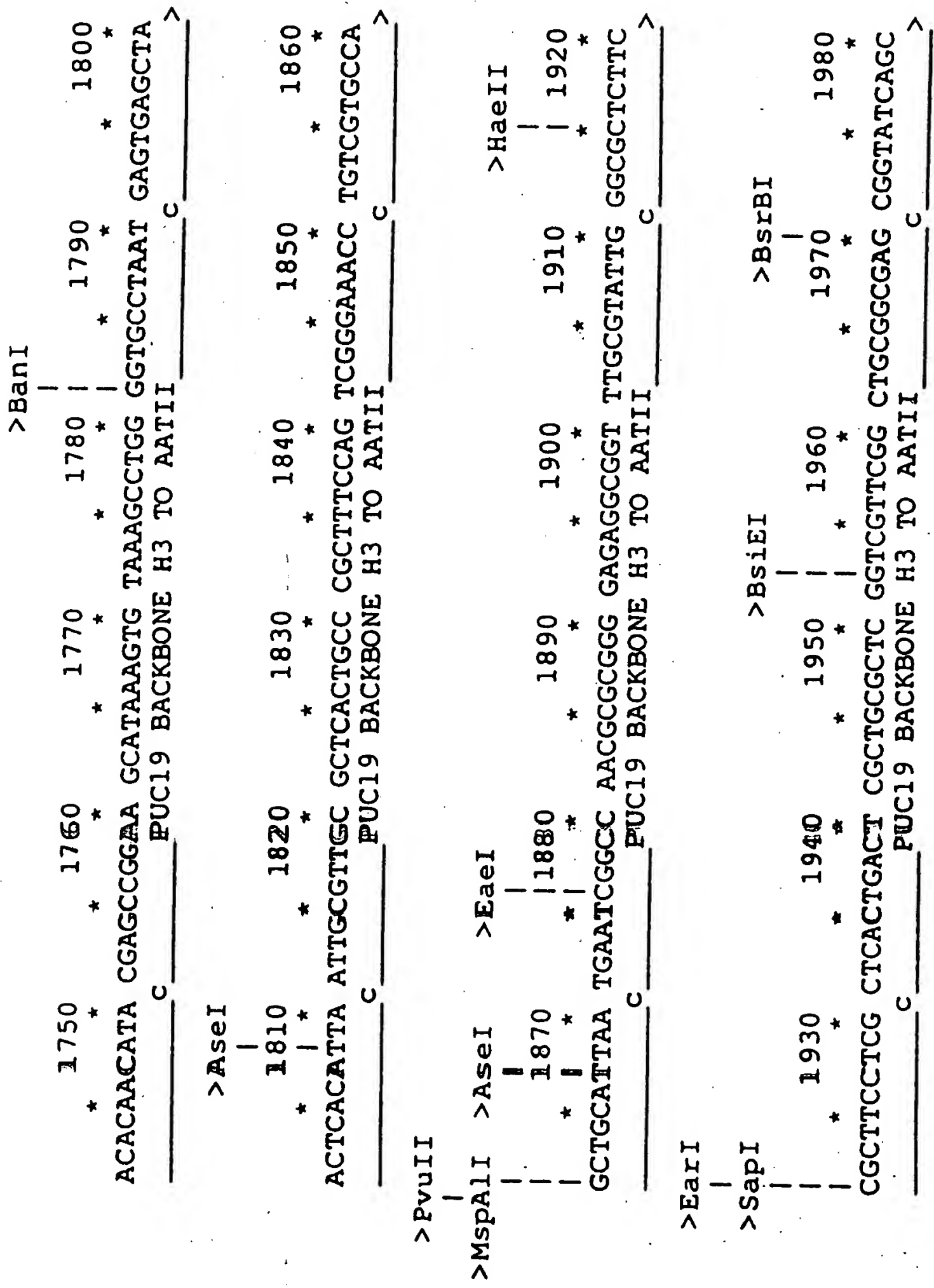


FIG. 4-10.



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>AflIII
1990 * 2000 2010 2020 2030 2040
* * * * *
TCACTCAAAG GCGGTAATAC GGTATCCAC AGAATCAGG GATAACGCAG GAAAGAACAT
C PUC19 BACKBONE H3 TO AATII C
2050 * 2060 2070 2080 2090 2100
* * * * *
GTGAGCAAAA GGCCAGCAA AGGCCAGGAA CCGTAAAAAG GCCGCGTGC TGGCGTTTT
C PUC19 BACKBONE H3 TO AATII C
>DrdI
2110 * 2120 2130 2140 2150 2160
* * * * *
CCATAGGCTC CGCCCCCTG ACGAGCATCA CAAAATCGA CGCTCAAGTC AGAGGTGGCG
C PUC19 BACKBONE H3 TO AATII C
>BssSI
2170 * 2180 2190 2200 2210 2220
* * * * *
AAACCCGACA GACTATAAA GATACCAGGC GTTCCCCCT GGAAGCTCCC TCGTGGGCTC
C PUC19 BACKBONE H3 TO AATII C
>BsaWl
2230 * 2240 2250 2260 2270 2280
* * * * *
TCCTGTTCCG ACCCTGCCGC TTACCGGATA CCTGTCCGCC TTCTCCCTT CGGAAGCGT
C PUC19 BACKBONE H3 TO AATII C

FIG 4-11.

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```
>HaeII          >SfcI
|               |
| 2290          | 2300 | 2310          | 2320          | 2330          | 2340
*              *   *   *   *           *   *           *   *
GGCGCTTCT CAATGCTCAC GCTGTAGGTA TCTCAGTTCG GTGTAGGTCG TTCGGCTCCAA
_____C_____PUC19 BACKBONE H3 TO AATII_____C_____>

>BsiHKAI      >MspAI
|               |
| 2350          | 2360          | 2370          | 2380          | 2390          | 2400
*              *   *   *   *           *   *           *   *
GCTGGGCTGT GTGCACGAAC CCCCCTTCA GCCCGACCGC TGGCCCTTAT CCGGTAATA
_____C_____PUC19 BACKBONE H3 TO AATII_____C_____>

>AlwNI
|               |
| 2410          | 2420          | 2430          | 2440          | 2450          | 2460
*              *   *   *   *           *   *           *   *
TCGTCTTGAG TCCAACCCGG TAAGACACGA CTTATCGCCA CTGGCAGCAG CCACTGGTAA
_____C_____PUC19 BACKBONE H3 TO AATII_____C_____>

>SfcI
|               |
| 2470          | 2480          | 2490          | 2500          | 2510          | 2520
*              *   *   *   *           *   *           *   *
CAGGATTAGC AGAGCGAGGT ATGTAGCGG TGCTACAGAG TTCTTGAAGT GGTGGCCTAA
_____C_____PUC19 BACKBONE H3 TO AATII_____C_____>
```

FIG. 4-12.



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+

2530 * 2540 * 2550 * 2560 * 2570 * 2580 *
CTACGGCTAC ACTAGAAGGA CAGTATTGG TATCTGCGCT CTGCTGAAGC CAGTTACCTT
C PUC19 BACKBONE H3 TO AATII C

>Eco57I

>MspAI

2590 * 2600 * 2610 * 2620 * 2630 * 2640 *
CGGAAAAAGA GTTGGTAGCT CTTGATCCGG CAAACAAACC ACCGCTGGTA GCGGTGGTTT
C PUC19 BACKBONE H3 TO AATII C

2650 * 2660 * 2670 * 2680 * 2690 * 2700 *
TTTTGTTGC AAGCAGCAGA TTACGCGCAG AAAAAGGA TCTCAAGAAG ATCCTTTGAT
C PUC19 BACKBONE H3 TO AATII C

>BspHI

2710 * 2720 * 2730 * 2740 * 2750 * 2760 *
CTTTTCTACG GGGTCTGACG CTCAGTGGA CGAAACTCA CGTTAAGGA TTTTGGTCAT
C PUC19 BACKBONE H3 TO AATII C

>DraI

>DraI

2770 * 2780 * 2790 * 2800 * 2810 * 2820 *
GAGATTATCA AAAAGGATCT TCACCTAGAT CCTTTTAAAT TAAAAATGAA GTTTTAAATC
C PUC19 BACKBONE H3 TO AATII C

FIG 4-13.



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>BamI
2830 * 2840 * 2850 * 2860 * 2870 * 2880 *
AATCTAAAGT ATATATGAGT AACTTGGTC TGACAGTTAC CAATGCTTAA TCAGTGAGGC
____c____PUC19 BACKBONE H3 TO AATII____a____AMP-ORF____>
____c____>

>AhdI
2890 * 2900 * 2910 * 2920 * 2930 * 2940 *
ACCTATCTCA GCGATCTGTC TATTTCGTC ATCCATAGTT GCCTGACTCC CCGTCGTGTA
____a____a____AMP-ORF____a____>
____c____PUC19 BACKBONE H3 TO AATII____c____>

>BsaI
>BsrDI >BpmI
2950 * 2960 * 2970 * 2980 * 2990 * 3000 *
GATAACTACG ATACGGGAGG GCTTACCATC TGGCCCCAGT GCTGCAATGA TACCGCGAGA
____a____a____AMP-ORF____a____>
____c____PUC19 BACKBONE H3 TO AATII____c____>

>BsrFI >BglI
3010 * 3020 * 3030 * 3040 * 3050 * 3060 *
CCCACGCTCA CCGGCTCCAG ATTTATCAGC AATAAACCCAG CCAGCCGGAA GGGCCGAGCG
____a____a____AMP-ORF____a____>
____c____PUC19 BACKBONE H3 TO AATII____c____>

FIG. 4-14.

+



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>AseI
3070 * 3080 * 3090 * 3100 * 3110 * 3120 *
CAGAAGTGGT CCTGCAACTT TATCCGCCTC CATCCAGTCT ATTAATTGTT GCCGGGAAGC
a a AMP-ORF a
c c PUC19 BACKBONE H3 TO AATII c

>PspI406I
>FspI | >BsrDI | >Sfcl
3130 * 3140 * 3150 * 3160 * 3170 * 3180 *
TAGAGTAAGT AGTTCGCCAG TTAATAGTTT GCGCAACGTT GTTGCCATTG CTACAGGCAT
a a AMP-ORF a
c c PUC19 BACKBONE H3 TO AATII c

>MslI
3190 * 3200 * 3210 * 3220 * 3230 * 3240 *
CGTGGTGTCG CGCTCGTCGT TTGGTATGGC TTCATTCAGC TCCGGTTCCC AACGATCAAG
a a AMP-ORF a
c c PUC19 BACKBONE H3 TO AATII c

FIG. 4-15.

+



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+

>PvuI
|
>BsiEI
|
3250 * 3260 * 3270 * 3280 * 3290 * 3300 *
GCGAGTTACA TGATCCCCCA TGTGTGCAA AAAAGCGGTT AGCTCCTTCG GTCCTCCGAT
a a AMP-ORF a a
c c PUC19 BACKBONE H3 TO AATII c c

>EaeI
|
>MslI
|
3310 * 3320 * 3330 * 3340 * 3350 * 3360 *
CGTTGTCAGA AGTAAGTTGG CCGCAGTGTT ATCACTCATG GTATGGCAG CACTGCATAA
a a AMP-ORF a a
c c PUC19 BACKBONE H3 TO AATII c c

>ScaI
|
3370 * 3380 * 3390 * 3400 * 3410 * 3420 *
TTCTCTTACT GTCATGCCAT CCGTAAGATG CTTTCTGTG ACTIGTGAGT ACTCAACCAA
a a AMP-ORF a a
c c PUC19 BACKBONE H3 TO AATII c c

>BsiEI
|
3430 * 3440 * 3450 * 3460 * 3470 * 3480 *
GTCATTCTGA GAATAGTGTA TCGGGCGACC GAGTTGCTCT TGCCCGGCGT CAATACGGGA
a a AMP-ORF a a
c c PUC19 BACKBONE H3 TO AATII c c

16.4-16.



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>XmnI
|
>PspI406I
|
>DraI >BsiHKAI
| 3510 3520 3530 3540
* * * *
TAATACCGCG CCACATAGCA GAACTTTAA AGTGCTCATC ATTGGAAAAC GTTCTTCGGG
a a AMP-ORF a
c c PUC19 BACKBONE H3 TO AATII c

>Eco57I
|
>ApaLI
|
>BssSI
| 3580 3590 3600
* * * *
GCGAAACTC TCAAGGATCT TACCGCTGTT GAGATCCAGT TCGATGTAAC CCACTCGTGC
a a AMP-ORF a
c c PUC19 BACKBONE H3 TO AATII c

>BsiHKAI
| 3610 3620 3630 3640 3650 3660
* * * * * *
ACCCAAGTGA TCTTCAGCAT CTTTACTTT CACCAGCGTT TCTGGGTGAG CAAAACAGG
a a AMP-ORF a
c c PUC19 BACKBONE H3 TO AATII c

FIG. 4-17.

+



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```
>MSLI
|
3670      3680      3690      3700      3710      3720
*      *      *      *      *      *
AAGGCAAAAT GCCGCAAAA AGGGAATAAG GCGACACGG AAATGTTGAA TACTCATACT
a      a      a      a      a      a
c      c      c      c      c      c
PUC19 BACKBONE H3 TO AATII >

>EarI      >SspI      >BspHI      >BsrBI
|      |      |      |
3730      3740      3750      3760      3770      3780
*      *      *      *      *      *
CTTCCTTTT CAATATTATT GAAGCATTTA TCAGGGTTAT TGTCTCATGA GCGGATACAT
c      c      c      c      c      c
PUC19 BACKBONE H3 TO AATII >

3790      3800      3810      3820      3830      3840
*      *      *      *      *      *
ATTGAATGT ATTTAGAAA ATAACAAT AGGGGTTCCG CGCACATTTC CCCGAAAAGT
c      c      c      c      c      c
PUC19 BACKBONE H3 TO AATII >

>HincII
|
>AccI
||
>AatII
||
>SalI
|||
3850 |||
* |||
GCCACCTGAC GTC
c      c      c
>
```

FIG 4-18.

+

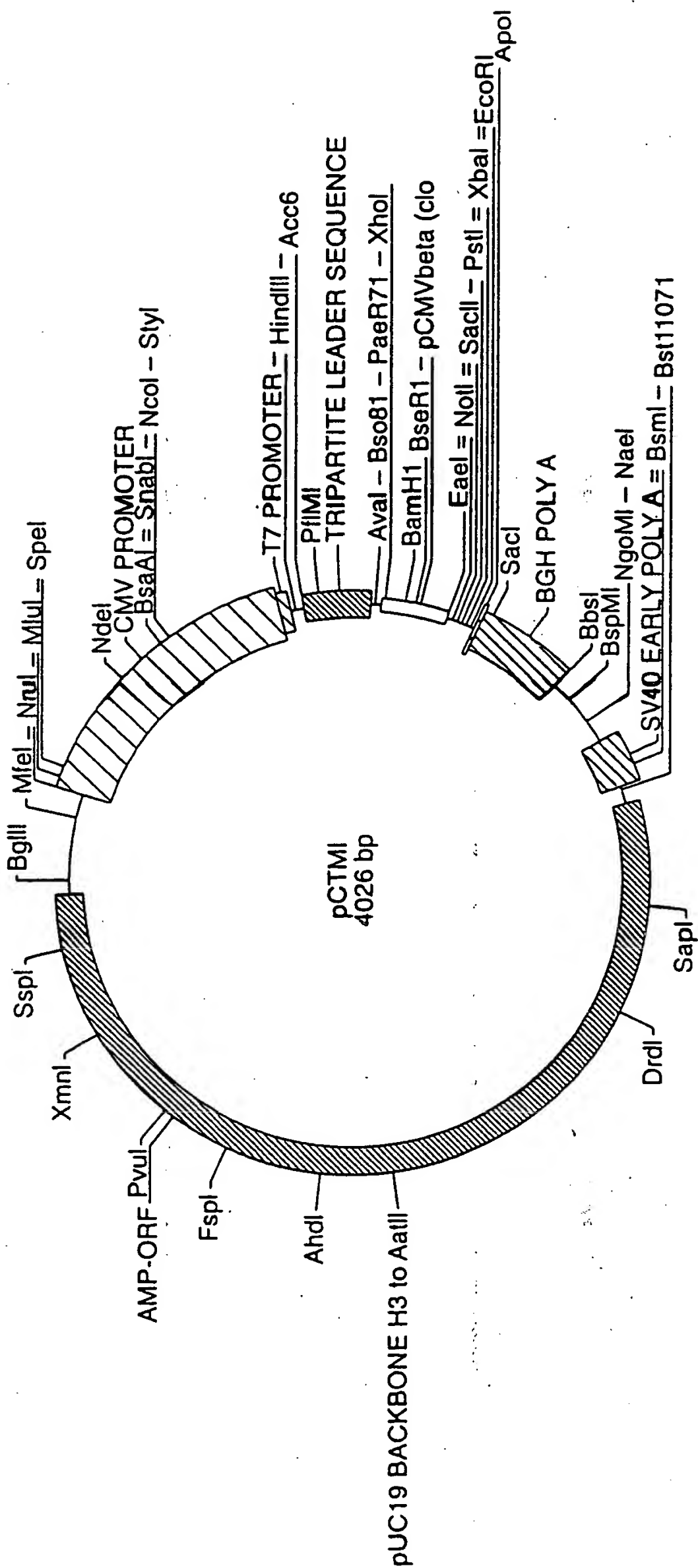


FIG. 5.



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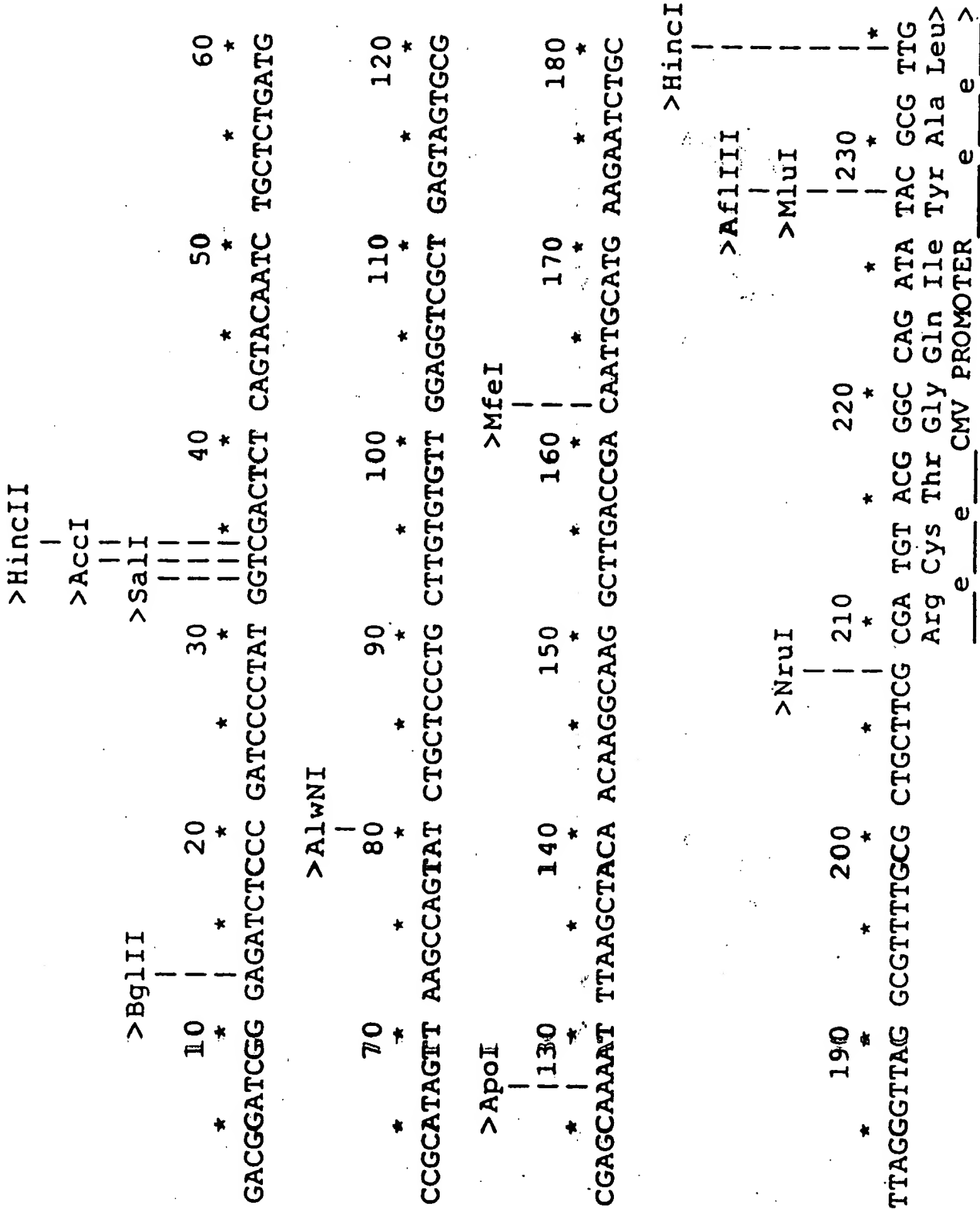


FIG. 6-1.

+



FIG. 6-2.

```

>AatII
|
430- *
| *
TCA ATG GGT GGA CTA TTT ACG GTA AAC TGC CCA CTT GGC AGT ACA TCA
Ser Met Gly Gly Leu Phe Thr Val Asn Cys Pro Leu Gly Ser Thr Ser>
e e e e e CMV PROMOTER e e e e e >

>BglI
|
440 *
| *
450 *
| *
460 *
| *
470 *
| *
TCA ATG GGT GGA CTA TTT ACG GTA AAC TGC CCA CTT GGC AGT ACA TCA
Ser Met Gly Gly Leu Phe Thr Val Asn Cys Pro Leu Gly Ser Thr Ser>
e e e e e CMV PROMOTER e e e e e >

>NdeI
|
480 *
| *
490 *
| *
500 *
| *
510 *
| *
520 *
| *
AGT GTA TCA TAT GCC AAG TAC GCC CCC TAT TGA CGT CAA TGA CGG TAA
Ser Val Ser Tyr Ala Lys Tyr Ala Pro Tyr *** Arg Gln *** Arg ***>
e e e e e CMV PROMOTER e e e e e >

>BglI
|
530 *
| *
540 *
| *
550 *
| *
560 *
| *
570 *
| *
ATG GCC CGC CTG GCA TTA TGC CCA GTA CAT GAC CTT ATG GGA CTT TCC
Met Ala Arg Leu Ala Leu Cys Pro Val His Asp Leu Met Gly Leu Ser>
e e e e e CMV PROMOTER e e e e e >

>BsaAI
|
580 *
| *
590 *
| *
600 *
| *
610 *
| *
TAC TTG GCA GTA CAT CTA CGT ATT AGT CAT CGC TAT TAC CAT GGT GAT
Tyr Leu Ala Val His Leu Arg Ile Ser His Arg Tyr Tyr His Gly Asp>
e e e e e CMV PROMOTER e e e e e >

>NcoI
|
>StyI >MslI
|
610 *
| *

```

FIG 6-3.

+



>AatII >BamI

720	730	740	750	760
* * *	* * *	* * *	* * *	* * *
GCA CCA AAA TCA ACG GGA CTT TCC AAA ATG TCG TAA CAA CTC CGC CCC				
Ala Pro Lys Ser Thr Gly Leu Ser Lys Met Ser *** Gln Leu Arg Pro>				
e e e e e	e e e e e	e e e e e	e e e e e	e e e e e

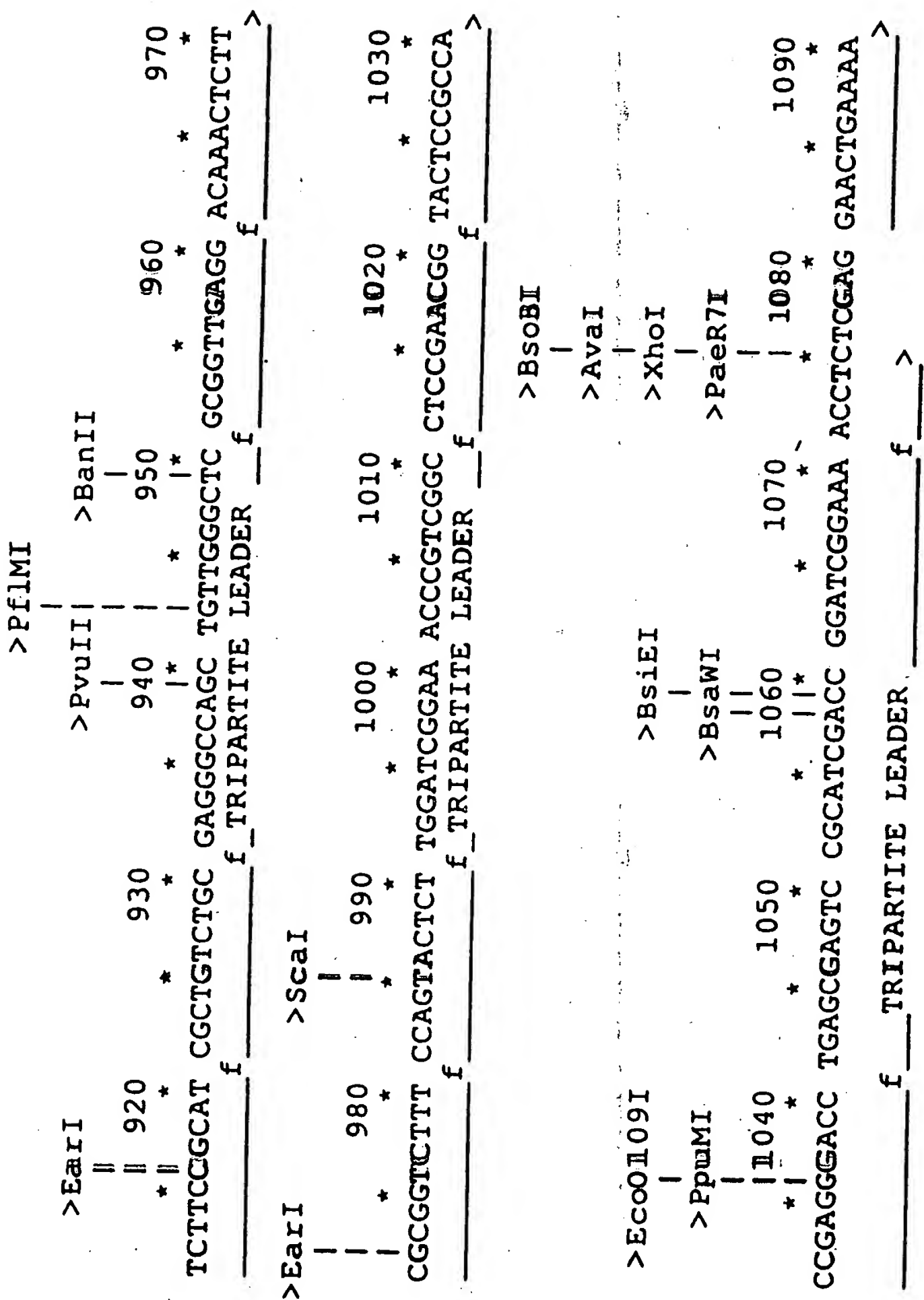
	770	780	790	800	810
*	*	*	*	*	*
ATT	GAC	GCA	AAT	GGG	CGG
CGG	TAG	GCG	TGT	ACG	GTG
GGT	GGA	GGT	CTA	TAT	AAG
Ala	Asn	Gly	Arg	**	Ala
Cys	Thr	Val	Gly	Gly	Leu
Tyr	Lys	>			
PROMOTER	e	e	e	e	e

FIG. 6-4.

+



+





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+

```
>HincII      >EcoOI09I  >BsaWI
|            |            |
>HpaI        >PpuMI   >BamHI
|            |            |
1100 |      1110      1120      1130      1140      1150
* |      * |      * |      * |      * |      * |
ACCAGAAAGT TAACTGGTAA GTTAGTCTT TTTGTCTTTT TATTCAGGT CCCGGATCCG
b          HYBRID SV40 LATE INTRON b
>BseRI      >StuI
|            |
1160 |      1170      1180      1190      1200      1210
* |      * |      * |      * |      * |      * |
GTGGTGGTGC AAATCAAAGA ACTGCTCCTC AGTGGATGTT GCCTTACTT CTAGGCCTGT
b          HYBRID SV40 LATE INTRON b
>BsiEI      >EagI      >EaeI      >SacII      >NotI      >SfcI      >XbaI
|            |            |            |            |            |
1220 |      1230      1240      1250      1260      1270
* |      * |      * |      * |      * |      * |
ACGGAAGTGT TACTTCTGCT CTAAAGCTG CGGAATGTA CCCGGGCCG CTGCAGTCTA
b          HYBRID SV40 LATE INTRON b
```

FIG 6-7.

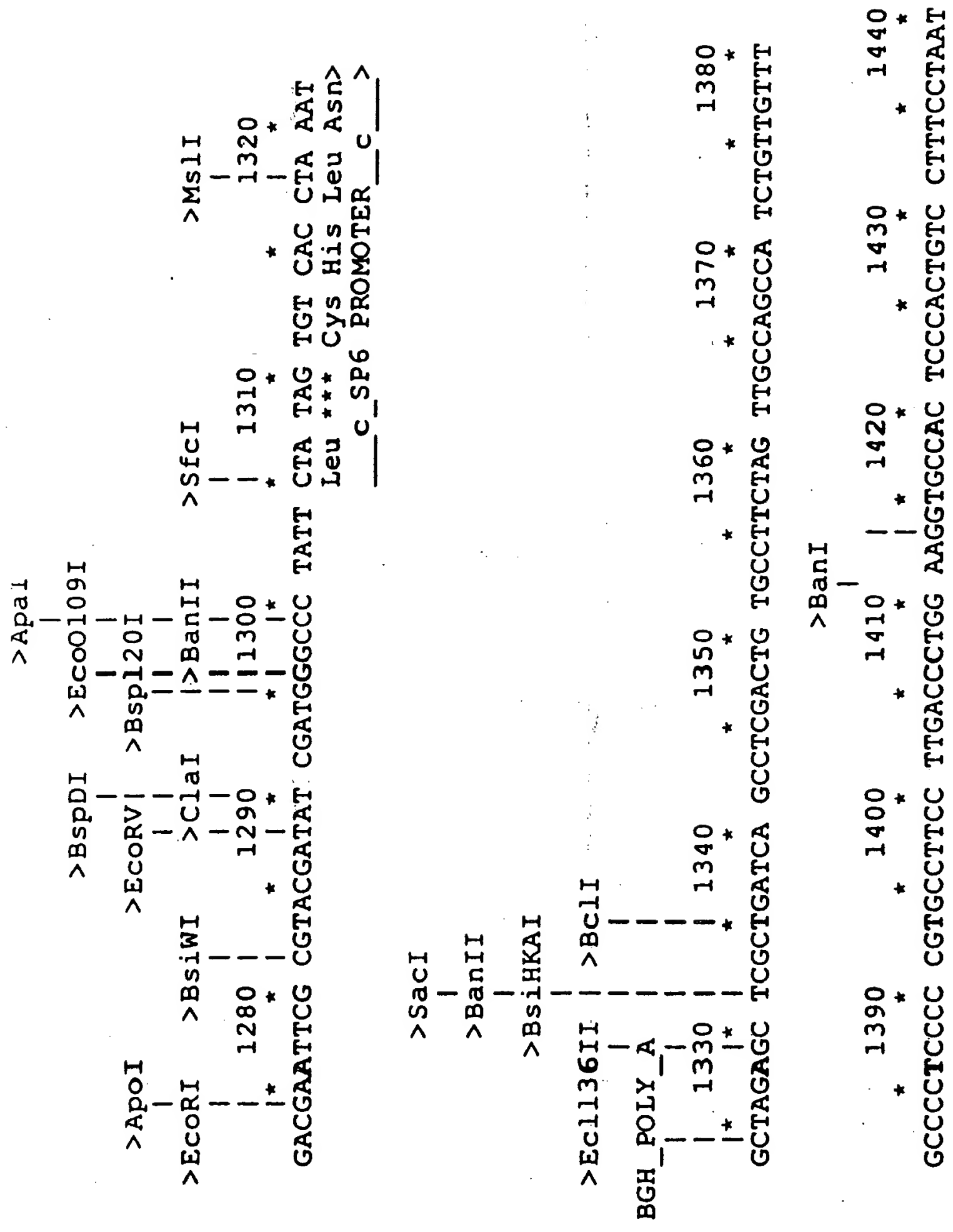


FIG. 6-8.

+

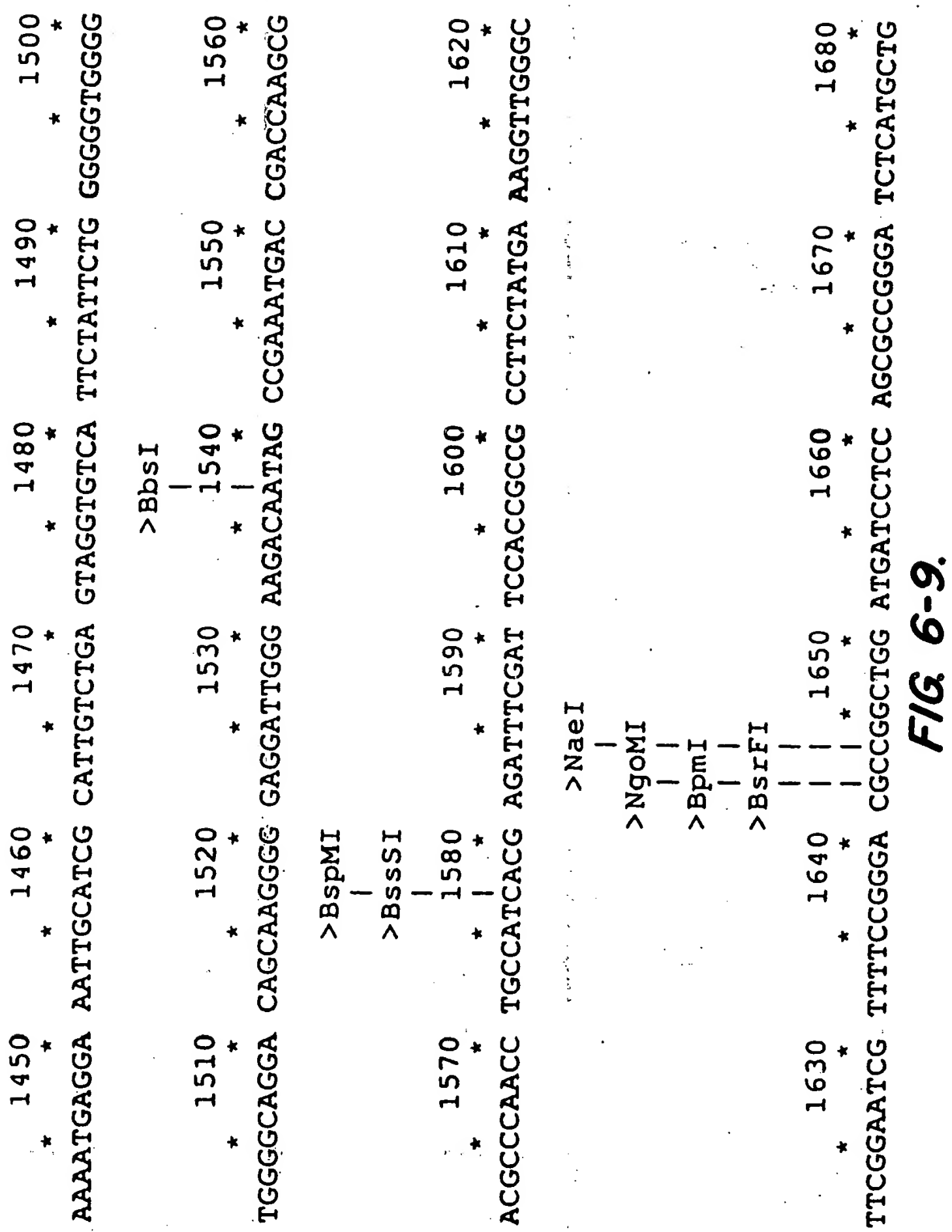


FIG 6-9.

+



```
>BpmI
|
>SV40_early_poly_A
1690 * 1700 1710 1720 1730 1740
* * * * *
GAGTTCTTCG CCCACCCCAA CTTGTTATT GCAGCTTATA ATGGTTACAA ATAAAGCAAT

>ApoI
|
1750 * 1760 1770 1780 1790 1800
* * * * *
AGCATCACAA ATTCACAAA TAAAGCATTT TTTCACTGC ATTCTAGTTG TGGTTGTCC

>HincII
|
>Bst1107I >AccI
| |
>AccI >SalI
| | |
1810 * 1820 1830 1840 1850 1860
* * * * *
AAACTCATCA ATGTATCTTA TCATGTCTGT ATACCGTCGA CCTCTAGCTA GAGCTTGGCG

>BsrBI
|
1870 * 1880 1890 1900 1910 1920
* * * * *
TAATCATGGT CATAGCTGTT TCCTGTGTGA AATTGTATC CGCTCACAAT TCCACACAAC
d d PUC19 BACKBONE d
```

FIG. 6-10.

+





+

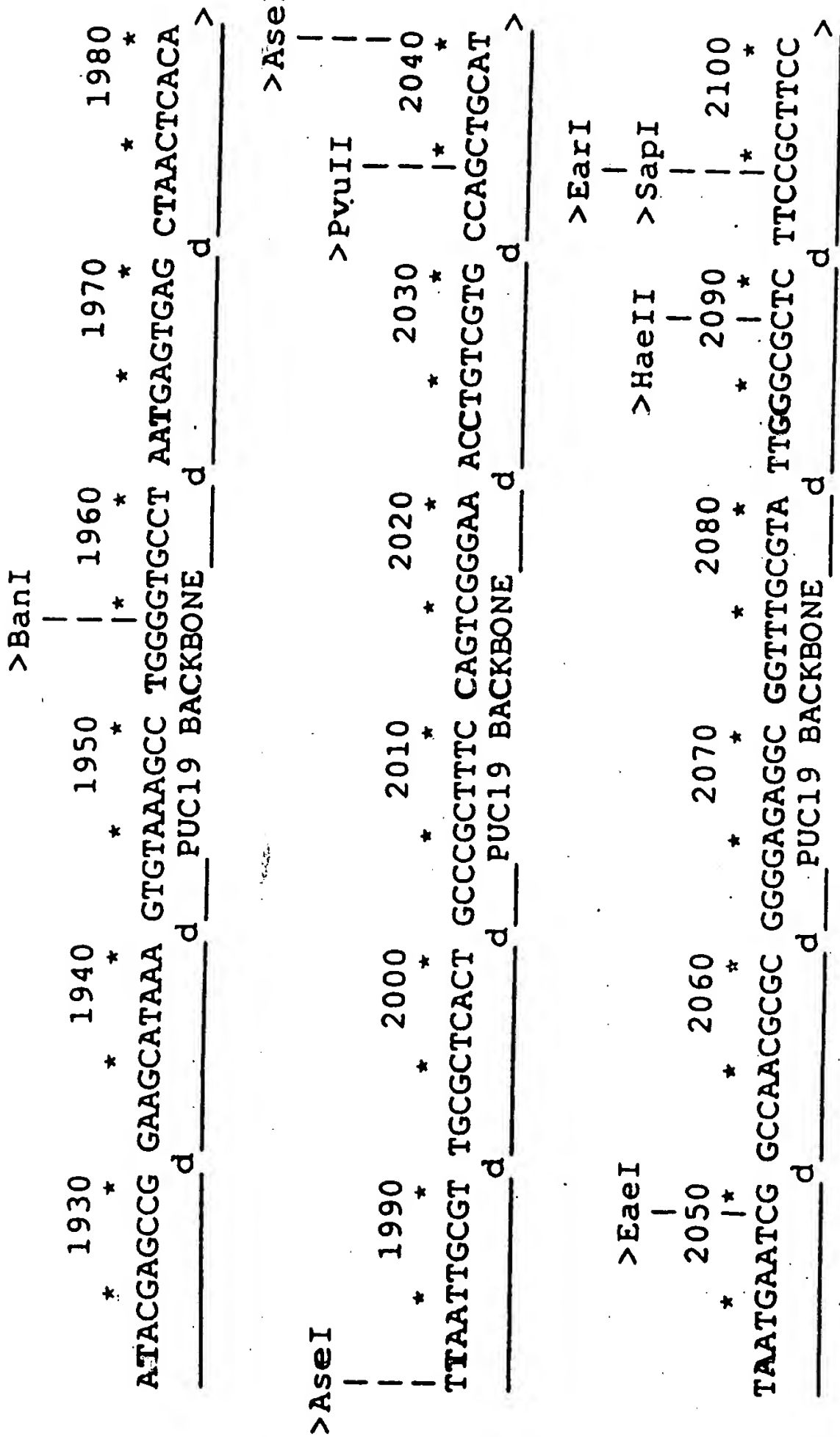


FIG. 6-11.



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```
>BsiEI
2110      2120      2130      2140      2150      2160
*      *      *      *      *      *
TCGCTCACTG ACTCGCTGCG CTGCGTCGTT CGGCTGCGGC GAGCGGTATC AGCTCACTCA
d      d      d      d      d      d
>BsrBI
2170      2180      2190      2200      2210      2220
*      *      *      *      *      *
AAGGCGGTAA TACGGTTATC CACAGAATCA GGGGATAACG CAGGAAAGAA CATGTGAGCA
d      d      d      d      d      d
>AflIII
2230      2240      2250      2260      2270      2280
*      *      *      *      *      *
AAAGGCCAGC AAAAGGCCAG GAACCGTAAA AAGGCCGCGT TGCTGGCGTT TTCCATAGG
d      d      d      d      d      d
>DrdI
2290      2300      2310      2320      2330      2340
*      *      *      *      *      *
CTCCGCCCCC CTGACGAGCA TCACAAAAT CGACGCTCAA GTCAGAGGTG GCGAAACCCG
d      d      d      d      d      d
>BssSI
2350      2360      2370      2380      2390      2400
*      *      *      *      *      *
ACAGGACTAT AAAGATACCA GCGGTTTCCC CCTGGAAGCT CCCTCGTGCG CTCTCCTGTT
d      d      d      d      d      d
```

FIG 6-12.

+



>BsaWI		>HaeII	
2410	2420	2430	2440
*	*	*	*
CCGACCCCTGC CGCTTACCGG ATACCTGTCC GCCTTCTCC CTCGGGAAG CGTGGCGCTT		PUC19 BACKBONE	
d	d	d	d
		>	
>SfcI			
2470	2480	2490	2500
*	*	*	*
TCTCAATGCT CACGCTGTAG GTATCTCAGT TCGGTGTAGG TCGTTCGCTC CAAGCTGGGC		PUC19 BACKBONE	
d	d	d	d
		>	
>BsiHKAI		>BsaWI	
>ApaLI		>BsiEI	
2530	2540	2550	2560
*	*	*	*
TGTGTGCACG AACCCCCCGT TCAGCCCGAC CGCTGCGCCT TATCCGGTAA CTATCGTCTT		PUC19 BACKBONE	
d	d	d	d
		>	
>AlwNI			
2590	2600	2610	2620
*	*	*	*
GAGTCCAACC CGGTAAGACA CGACTTATCG CCACTGGCAG CAGCCACTGG TAACAGGATT		PUC19 BACKBONE	
d	d	d	d
		>	

FIG. 6-13.

+



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>Sfci
2650 2660 2670 2680 2690 2700
* * * * *
AGCAGAGCGA GGTATGTAGG CGGTGCTACA GAGTCTTGA AGTGGTGGCC TAACTACGGC
d d PUC19 BACKBONE d
>
>Eco57I
2710 2720 2730 2740 2750 2760
* * * * *
TACACTAGAA GGACAGTATT TGGTATCTGC GCTCTGCTGA AGCCAGTTAC CTTCGGAAAA
d d PUC19 BACKBONE d
>
2770 2780 2790 2800 2810 2820
* * * * *
AGAGTTGGTA GCTCTTGATC CGGCAAAACA ACCACCGCTG GTAGCGGTGG TTTTITTTGTT
d d PUC19 BACKBONE d
>
2830 2840 2850 2860 2870 2880
* * * * *
TGCAAGCAGC AGATTACGCG CAGAAAAAA GGATCTCAAG AAGATCCTT GATCTTTTCT
d d PUC19 BACKBONE d
>
>BspHI
2890 2900 2910 2920 2930 2940
* * * * *
ACGGGTCTG ACGCTCAGTG GAACGAAAC TCACGTTAAG GGATTTGGT CATGAGATTA
d d PUC19 BACKBONE d
>

FIG 6-14.

+



+

>DraI >DraI
| |
2950 2960 2970 2980 2990 3000
* * * * * *
TCAAAAGGA TCTTCACCTA GATCCTTTA AATTAAAAAT GAAGTTTAA ATCAATCTAA
d d PUC19 BACKBONE d d

>BamI
|
3010 3020 3030 3040 3050 3060
* * * * * *
AGTATATATG AGTAAACTTG GTCTGACAGT TACCAATGCT TAATCAGTGA GGCACCTATC
AMP-ORF a
d d PUC19 BACKBONE d d

>AhdI
| |
3070 3080 3090 3100 3110 3120
* * * * * *
TCAGCGATCT GTCTATTTCG TTCATCCATA GTTGCCCTGAC TCCCCGTCGT GTAGATAACT
AMP-ORF a
d d PUC19 BACKBONE d d

>BsaI >BsrDI >BpmI
| | |
3130 3140 3150 3160 3170 3180
* * * * * *
ACGATACGGG AGGGCTTACC ATCTGGCCCC AGTGCTGCAA TGATACCGCG AGACCCACGC
AMP-ORF a
d d PUC19 BACKBONE d d

FIG. 6-15.



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+

>BsrFI | | 3190 3200 3210 3220 3230 3240
| * | * | * | * | *
TCACCGGCTC CAGATTATC AGCAATAAC CAGCCAGCCG GAAGGGCCGA GCGCAGAAGT
a a AMP-ORF a
d d PUC19 BACKBONE d d

>AseI | | 3270 3280 3290 3300
| * | * | * | *
GGTCCCTGCAA CTTATCCGC CTCCATCCAG TCTATTAATT GTTGCCGGGA AGCTAGAGTA
a a AMP-ORF a
d d PUC19 BACKBONE d d

>Psp1406I | | 3330 3340 3350 3360
| * | * | * | *
AGTAGTTCGC CAGTTAATAG TTGCGCAAC GTTGTGCCA TTGCTACAGG CATCGTGGTG
a a AMP-ORF a
d d PUC19 BACKBONE d d

FIG 6-16.



>BsāWI
3370 * 3380 * 3390 * 3400 * 3410 * 3420 *
TCACGCTCGT CGTTTGAT GGCTTCATC AGCTCCGGT CCCAACGATC AAGGCGAGTT
a AMP-ORF a
d PUC19 BACKBONE d

>BsiEI
3430 * 3440 * 3450 * 3460 * 3470 * 3480 *
ACATGATCCC CCATGTTGTG CAAAAGCG GTAGCTCCT TCGGTCCTCC GATCGTTGTC
a AMP-ORF a
d PUC19 BACKBONE d

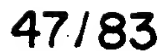
>EaeI
3490 * 3500 * 3510 * 3520 * 3530 * 3540 *
AGAAGTAAGT TGGCCGCAGT GTATCACTC ATGGTTATGG CAGCACTGCA TAATTCTCTT
a AMP-ORF a
d PUC19 BACKBONE d

>ScaI
3500 * 3560 * 3570 * 3580 * 3590 * 3600 *
ACTGTCATGC CATCCGTAAG ATGCTTTTCT GTGACTGGTG AGTACTCAAC CAAGTCATTC
a AMP-ORF a
d PUC19 BACKBONE d

FIG. 6-17.

+

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	>MslI		>EarI	
3850	3860	3870	3880	3900
*	*	*	*	*
AATGCCGCAA	AAAAGGGAAT	AAGGGCGACA	CGGAAATGTT	GAATACTCAT
a	a	AMP-ORF	a	ACTCTTCCTT
d	d	PUC19 BACKBONE	d	>

>SspI	>BspHI	>BsrBI	
3910	3940	3950	3960
* *	* *	* *	* *
TTTCAATATT	TTATCAGGGT	TATTGTCTCA	TGAGCGGATA CATATTGAA
d	d	d	d
PUC19	BACKBONE		
			>

FIG. 6-19.

+



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+

```
3970      *      3980      *      3990      *      4000      *      4010      *      4020      *
      *      *      *      *      *      *      *      *      *
TGTAATTAGA AAAATAAACA AATAGGGGTT CCGCGCACAT TTCCCCGAAA AGTGCCACCT
      d      d      PUC19 BACKBONE      d      d      d      d      d      d
>HincII
      |
>AatII
      ||
>AccI
      ||
>SalI
      |||
      |*|
GACGTC
      >
```

FIG. 6-20.

|||||

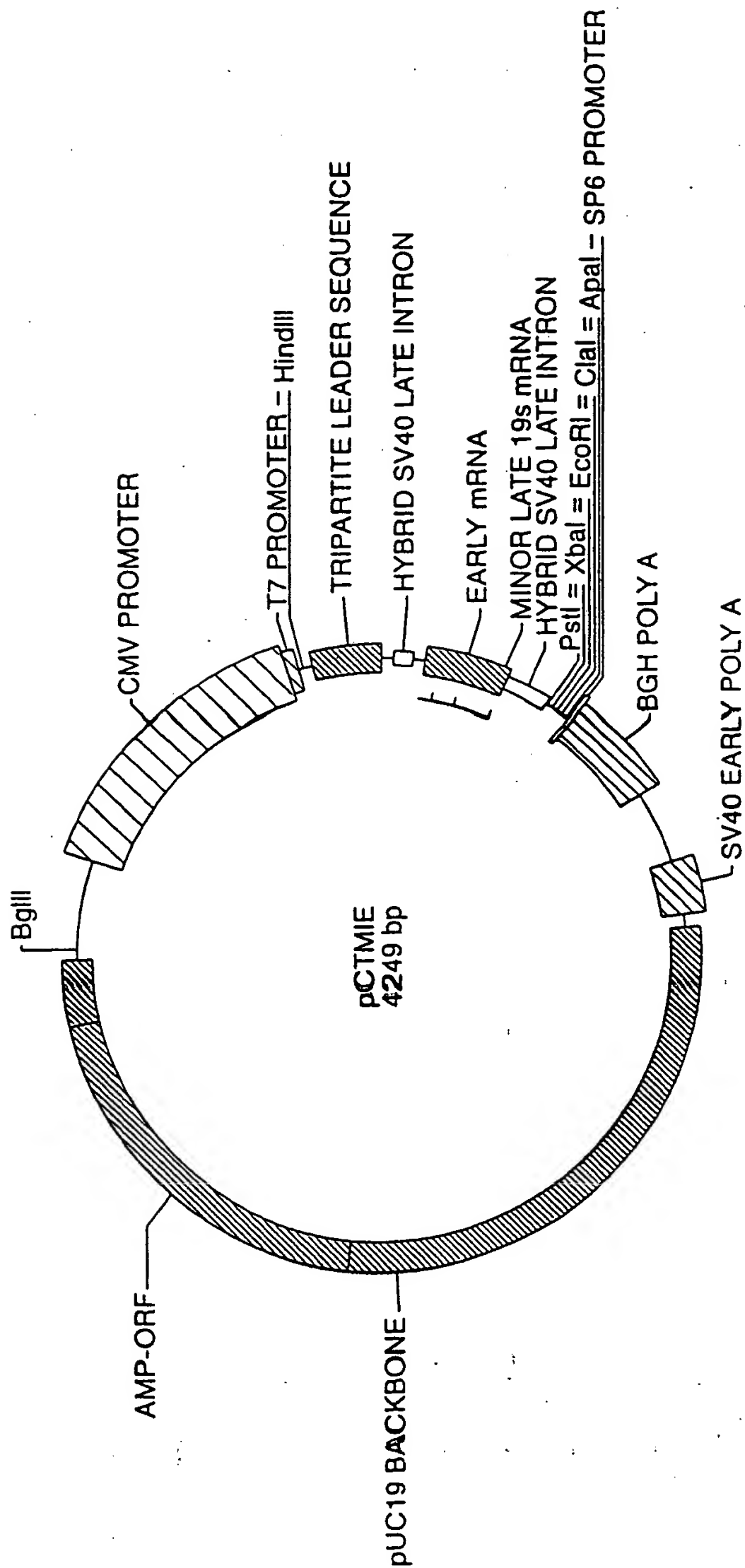


FIG. 7.

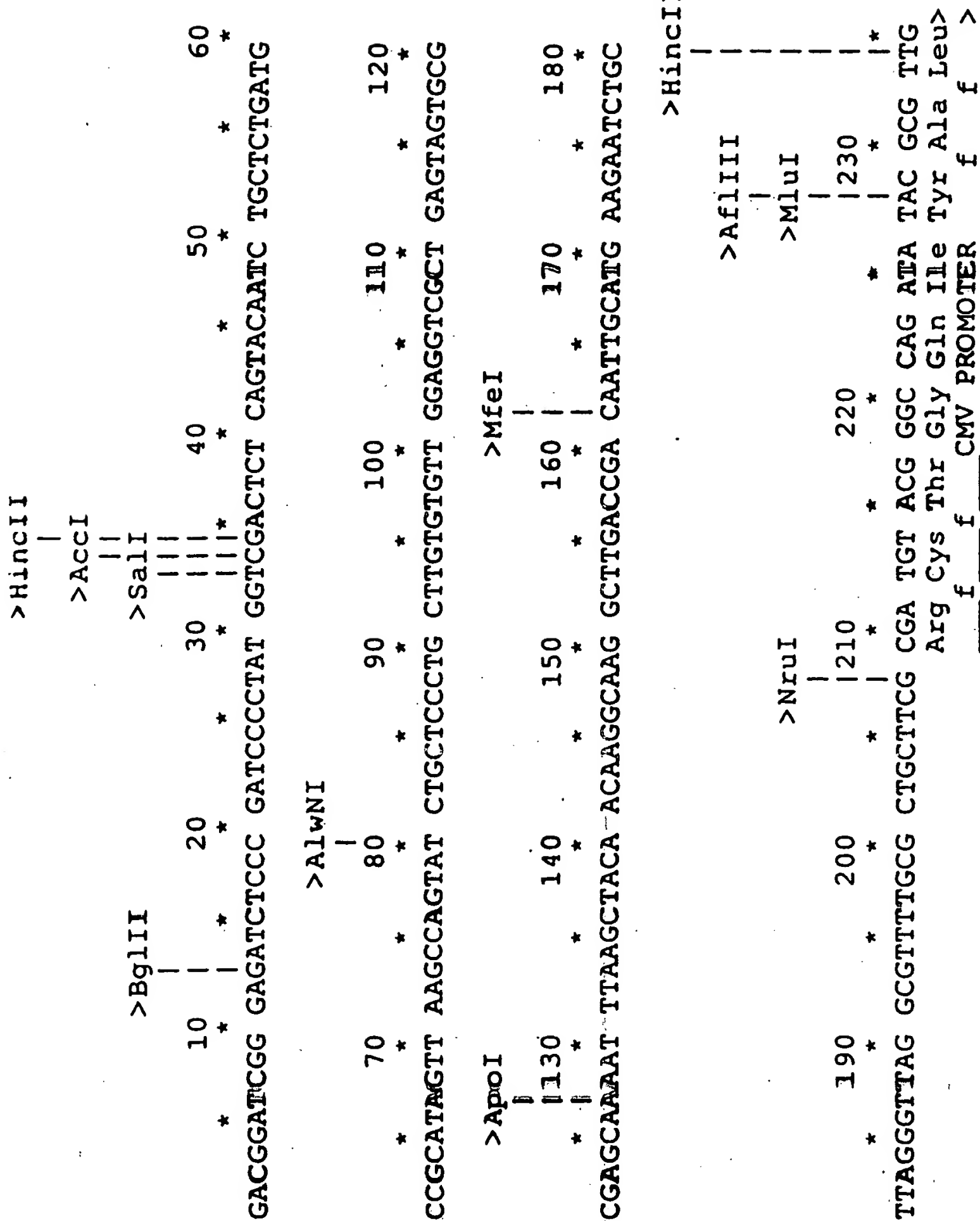


FIG. 8-1.

+



FIG. 8-2:

+

[illegible][illegible][illegible][illegible]

FIG. 8-3.

+



	>AatII			>BamI
670 *		680 *	690 *	
GGG ATT TCC AAG TCT CCA CCC CAT TGA CGT CAA TGG GAG TTT GTT TTG		*	*	710 *
Gly Ile Ser Lys Ser Pro Pro His ** Arg Gln Trp Glu Phe Val Leu>		f f f f CMV PROMOTER f f f f f f f >		

[illegible]

	770	780	790	800	810
*	*	*	*	*	*
ATT	GAC	GCA	AAT	GGG	CGG
	TAG	GCG	TGT	ACG	GTG
	GGA	GGT	CTA	TAT	AAG
Ile	Asp	Ala	Asn	Gly	Arg
	***	Ala	Cys	Thr	Val
	Gly	Gly	Gly	Gly	Leu
	Tyr	Lys	>		
f	f	f	f	f	f
	CMV	PROMOTER			

FIG. 8-4.



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```
>EarI      >PflMI
|          |
| 920      | 940      | 950      | 960      | 970
* | *      | * | *      | * | *      | * | *
TCTTCCGCAT CGCTGTCTGC GAGGGCCAGC TGTGGGCTC GCGTTGAGG ACAAACTCTT
_____g_____TRIPARTITE LEADER SEQUENCE_____g_____>

>EarI      >ScaI
|          |
| 980      | 990      | 1000     | 1010     | 1020     | 1030
* | *      | * | *      | * | *      | * | *      | * | *
CGCGGTCTTT CCAGTACTCT TGGATCGGAA ACCGTCGGC CTCGGAACGG TACTCCGCCA
_____g_____TRIPARTITE LEADER SEQUENCE_____g_____>

>XhoI
|
>AvaI
|
>BsoBI
|
>PaeR7I
|
>EcoO109I  >BsiEI
|          |
>PpuMI     |
|          |
| 1040      | 1050      | 1060      | 1070      | 1080      | 1090
* | *      | * | *      | * | *      | * | *      | * | *
CCGAGGGACC TGAGCGAGTC CGCATCGACC GGATCGGAAA ACCTCTCGAG GAACTGAAAA
```

FIG 8-6.

+

TRIPARTITE LEADER SEQUENCE _____ g _____ >

[illegible]

```

>Ppul0I
|
>21_bp_tandem_repeat_III_[110],[102],[112]
|
1160 * 1170 1180 1190 1200 1210
AGTTAGGGCG GGACATGGGC GGAGTTAGGG GCGGGA CTA T GGTCGTGAC TAATTGAGAT
* * * * *
< _____ h EARLY MRNA _____ h

```

```
>SphI  
|  
>NsiI | | | | |  
| | | | |  
| | | | |  
| | | | |  
| * | 1220 * 1230 * 1240 * 1250 * 1260 * 1270 *  
  
GCATGCTTGG CATACTTC TG CCTGCTGGGG AGCCTGGGGA CTTCCACAC CTGGTTGCTG  
< _____ h _____ h _____ h
```

FIG. 8-7.

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1570 * 1580 * 1590 * 1600 * 1610 * 1620 *
TCAGCCTCGA CTGTGCCTTC TAGTTGCCAG CCATCTGTTG TTTGCCCCCTC CCCC GTGCCT

>BspMI
|
1630 * 1640 * 1650 * 1660 * 1670 * 1680 *
TCCTTGACCC TGGAGGGTGC CACTCCCACT GTCCTTTCCT AATAAAATGA GGAAATTGCA

1690 * 1700 * 1710 * 1720 * 1730 * 1740 *
TCGCATTGTC TGAGTAGGTG TCATTCTATT CTGGGGGGTG GGTGGGGCA GGACAGCAAG

>BbsI
|
1750 * 1760 * 1770 * 1780 * 1790 * 1800 *
GGGGAGGATT GGGAAGACAA TAGCCGAAT GACCGACCAA GCGACGCCCA ACCTGCCATC

1810 * 1820 * 1830 * 1840 * 1850 * 1860 *
ACGAGATTTC GATTCACCG CCGCCTTCTA TGAAGGTTG GGCTTCGGAA TCGTTTCCG

FIG 8-10.

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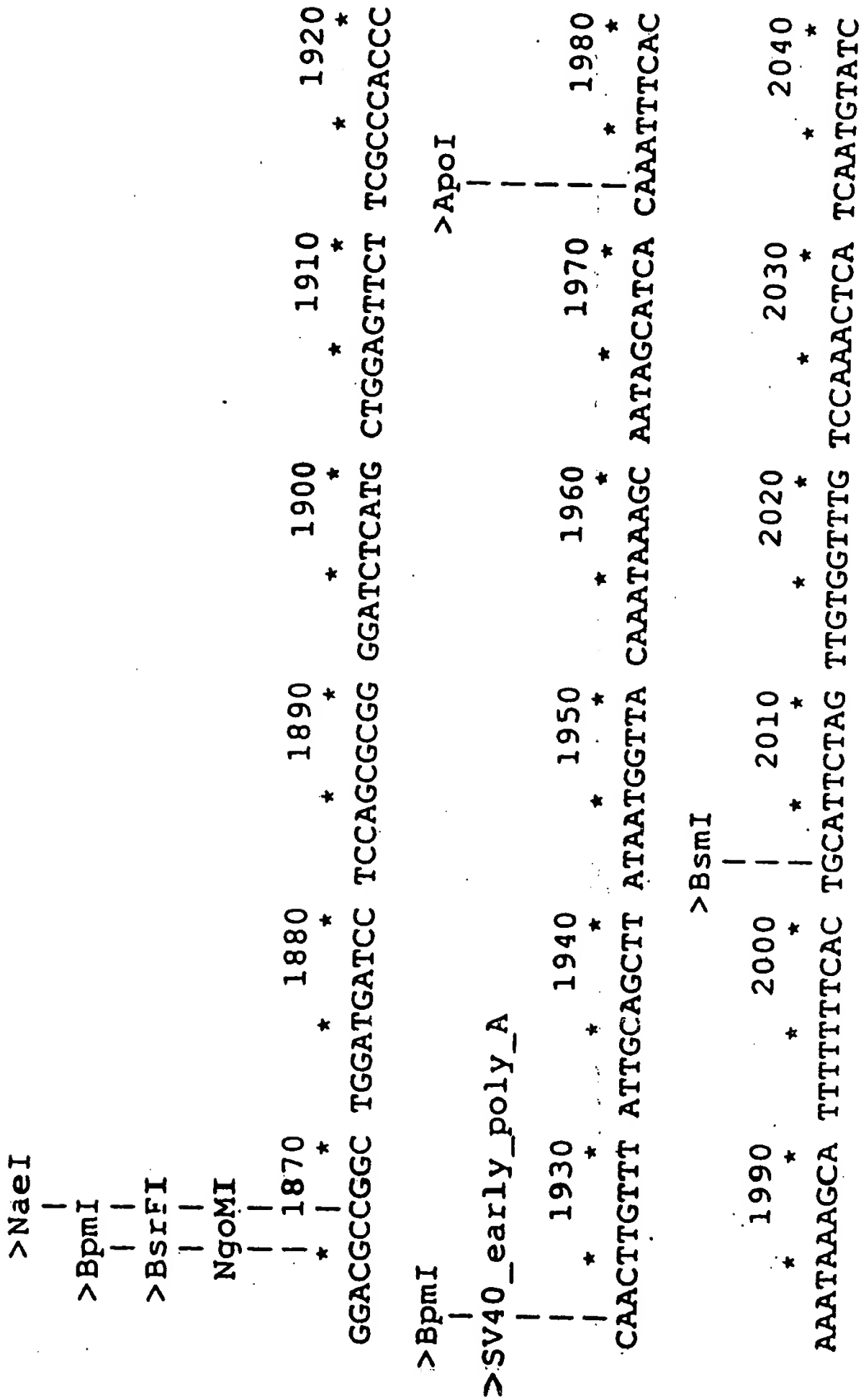


FIG. 8-II.

+

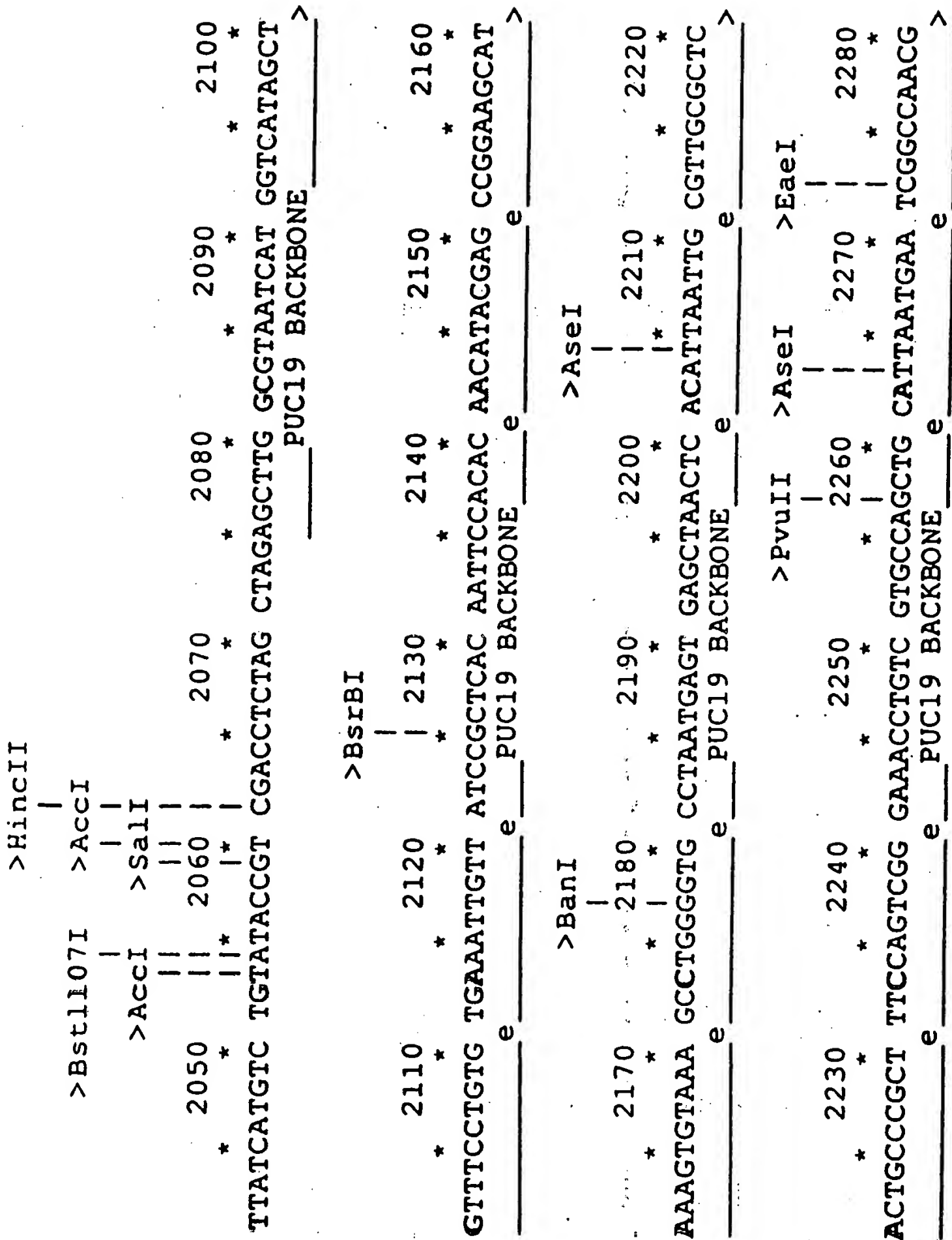


FIG 8-12.

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>SapI

>HaeII

>EaRI

2290 * 2300 2310 2320 2330 2340

* * * * *

CGCGGGGAGA GCGGGTTGC GTATTGGCG CTCTTCGCT TCCTCGCTCA CTGACTCGCT

e PUC19 BACKBONE e

>BsiEI

>BsrBI

2350 2360 2370 2380 2390 2400

* * * * *

GCGCTCGGTC GTTCGGCTGC GCGAGCGGT ATCAGCTCAC TCAAAGGCGG TAATACGGTT

e PUC19 BACKBONE e

>AflIII

2410 2420 2430 2440 2450 2460

* * * * *

ATCCACAGAA TCAGGGGATA ACGCAGGAAA GAACATGTGA GCAAAGGCC AGCAAAGGC

e PUC19 BACKBONE e

2470 2480 2490 2500 2510 2520

* * * * *

CAGGAACCGT AAAAAGGCCG CGTTGCTGGC GTTTTCCAT AGGCTCCGCC CCCCTGACGA

e PUC19 BACKBONE e

FIG. 8-13.

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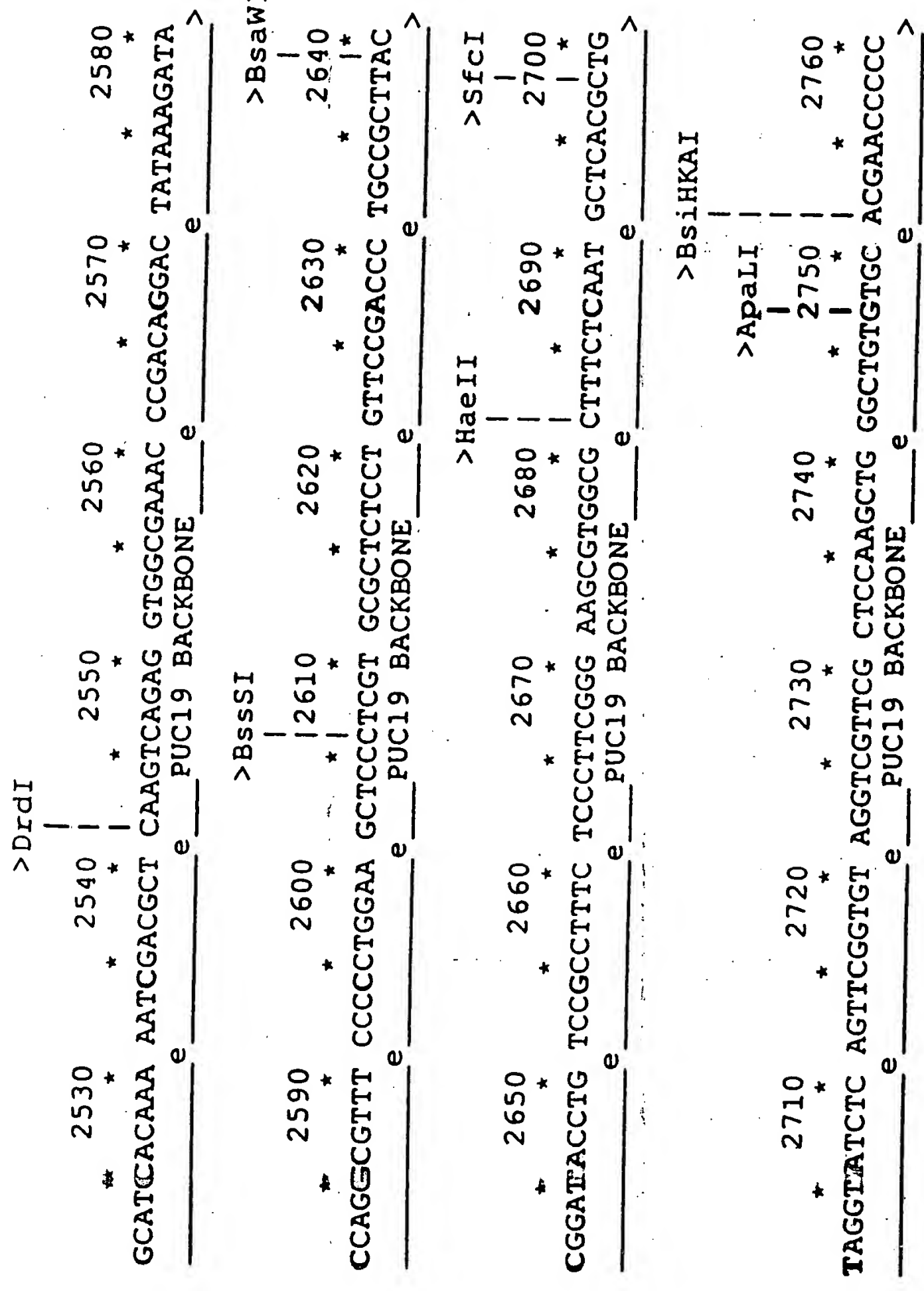


FIG. 8-14.





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```
>BsiEI          >BsaWI
|               |
2770 *          | 2780 *          | 2790 *          | 2800 *          | 2810 *          | 2820 *
*          *          *          *          *          *          *
CGTTCAGCCC GACCGCTGCG CCTATCCGG TAACTATCGT CTTGAGTCCA ACCCGGTAAG
e          e          e          e          e          e          e
PUC19 BACKBONE                                     >

>AlwNI
|
2830 *          | 2840 *          | 2850 *          | 2860 *          | 2870 *          | 2880 *
*          *          *          *          *          *          *
ACACGACTTA TCGCCACTGG CAGCAGCCAC TGGTAACAGG ATTAGCAGAG CGAGGTATGT
e          e          e          e          e          e          e
PUC19 BACKBONE                                     >

>Sfci
|
2890 *          | 2900 *          | 2910 *          | 2920 *          | 2930 *          | 2940 *
*          *          *          *          *          *          *
AGGCGGTGCT ACAGAGTTCT TGAAGTGGTG GCCTAACTAC GGCTACACTA GAAGGACAGT
e          e          e          e          e          e          e
PUC19 BACKBONE                                     >

>Eco57I
|
2950 *          | 2960 *          | 2970 *          | 2980 *          | 2990 *          | 3000 *
*          *          *          *          *          *          *
ATTGGTATC TGGGCTCTGC TGAAGCCAGT TACCTTCGGA AAAAGAGTTG GTAGCTCTTG
e          e          e          e          e          e          e
PUC19 BACKBONE                                     >
```

FIG 8-15.



[illegible]

FIG. 8-16.

+

>AhdI
3310 * 3320 * 3330 * 3340 * 3350 * 3360 *
TCGTTCAATCC ATAGTTGCCT GACTCCCCGT CGTGTAGATA ACTACGATAC GGGAGGGCTT
a e a AMP-ORF a a
e e PUC19 BACKBONE e e

>BsaI
>BsrDI >BpmI >BsrFI
3370 * 3380 * 3390 * 3400 * 3410 * 3420 *
ACCATCTGGC CCCAGTGCTG CAATGATACC GCGAGACCCA CGCTCACCGG CTCAGATT
a e a AMP-ORF a a
e e PUC19 BACKBONE e e

>BglI
3430 * 3440 * 3450 * 3460 * 3470 * 3480 *
ATCAGCAATA AACGAGCCAG CCGGAAGGC CGAGCGCAGA AGTGGTCTG CAACTTATC
a e a AMP-ORF a a
e e PUC19 BACKBONE e e

FIG. 8-17.

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>AseI
3490 * 3500 * 3510 * 3520 * 3530 * 3540 *
CGCCTCCATC CAGTCTATTA ATTGTTGCCG GGAAGCTAGA GTAAGTAGTT CGCCAGTTAA
a AMP-ORF a
e PUC19 BACKBONE e

>PspI406I
>EspI | >BsrDI | >SfcI | >MslI
3550 | 3560 | 3570 | 3580 | 3590 | 3600 |
* | * | * | * | * | * |
TAGTTTGGCG AACGTTGTTG CCATTGCTAC AGGCATCGTG GTGTCACGCT CGTCGTTTGG
a AMP-ORF a
e PUC19 BACKBONE e

>BsaWI
3610 * 3620 * 3630 * 3640 * 3650 * 3660 *
TATGGCTTCA TTCAGCTCCG GTTCCCAACG ATCAAGGCGA GTTACATGAT CCCCCATGTT
a AMP-ORF a
e PUC19 BACKBONE e

>BsiEI | >PvuI | >EaeI
3670 * 3680 * 3690 * 3700 * 3710 * 3720 *
GTGCAAAA GCGGTTAGCT CCTTCGGTCC TCCGATCGTT GTCAGAAGTA AGTTGGCCGC
a AMP-ORF a
e PUC19 BACKBONE e

FIG. 8-18.

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```
>MslI
3730 * 3740 3750 3760 3770 3780
AGTGTTATCA CTCATGGTTA TGGCAGCACT GCATAATTCT CTTACTGTCA TGCCATCCGT
a e a AMP-ORF a a
e e PUC19 BACKBONE e e

>ScaI
3790 3800 3810 3820 3830 3840
AAGATGCTTT TCTGTGACTG GTGAGTACTC AACCAAGTCA TTCTGAGAAT AGTGTATGCG
a a AMP-ORF a a
e e PUC19 BACKBONE e e

>BsiEI
3850 3860 3870 3880 3890 3900
GCGACCGAGT TGCTCTTGCC CGGCGTCAAT ACGGGATAAT ACCGGGCCAC ATAGCAGAAC
a a AMP-ORF a a
e e PUC19 BACKBONE e e

>PspI406I
3910 3920 3930 3940 3950 3960
TTTAAAGTG CTCATCATTTG GAAACGCTC TTCGGGGCGA AAACCTCTCAA GGATCTTACC
a a AMP-ORF a a
e e PUC19 BACKBONE e e

>DraI >BsiHKAI >XmnI
3910 3920 3930 3940 3950 3960
TTTAAAGTG CTCATCATTTG GAAACGCTC TTCGGGGCGA AAACCTCTCAA GGATCTTACC
a a AMP-ORF a a
e e PUC19 BACKBONE e e
```

FIG. 8-19.



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>Eco57I
|
>ApaLI
|
>BssSI |>BsiHKAI
| |
3970 * 3980 * 3990 * 4000 * 4010 * 4020 *
GCTGTTGAGA TCCAGTTCGA TGTAACCCAC TCGTGACCC AACTGATCTT CAGCATCTTT
a a AMP-ORF a a
e e PUC19 BACKBONE e e
>
>

4030 * 4040 * 4050 * 4060 * 4070 * 4080 *
TACTTTCACC AGCGTTTCTG GGTGAGCAA AACAGGAAGG CAAATGCCG CAAAAGGG
a a AMP-ORF a a
e e PUC19 BACKBONE e e
>
>

>MslI
||
4090 * 4100 * 4110 * 4120 * 4130 * 4140 *
AATAAGGCG ACACGGAAAT GTTGAATACT CATACTCTC CTTTTCAT ATTATTGAAG
a a AMP-ORF a a
e e PUC19 BACKBONE e e
>
>

FIG. 8-20.

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```
>BspHI      >BsrBI
|            |
4150  *      4160  |      4170  *      4180  *      4190  *      4200  *
      *      *      *      *      *      *
CATTATCAG GGTATTGTC TCATGAGCGG ATACATATTT GAATGTATTT AGAAAAATAA
      e      e      e      e      e      e
      PUC19 BACKBONE      PUC19 BACKBONE      PUC19 BACKBONE      PUC19 BACKBONE
      >      >      >      >      >      >

>HincII
|
>AccI
||
>AatII
||
>SalI
|||
|||
|||
|||
4210  *      4220  *      4230  *      4240  *
      *      *      *      *
ACAAATAGGG GTTCCGCGCA CATTTCCTCCG AAAAGTGCCA CCTGACGTC
      e      e      e      e
      PUC19 BACKBONE      PUC19 BACKBONE      PUC19 BACKBONE      PUC19 BACKBONE
      >      >      >      >
```

FIG. 8-21.

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95 194 286 437

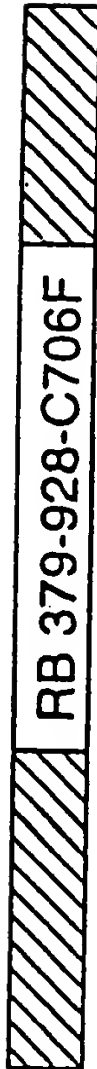
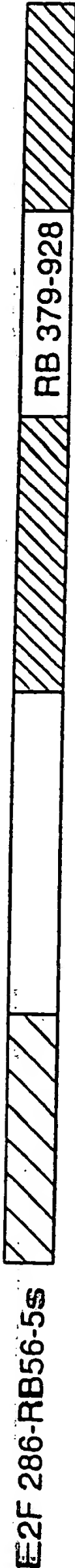
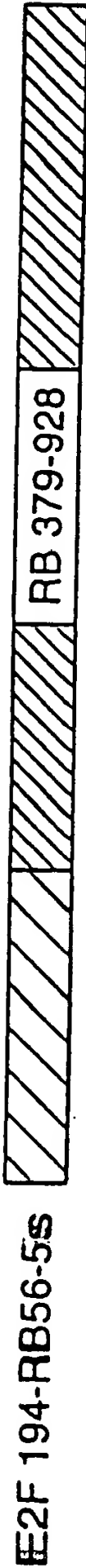
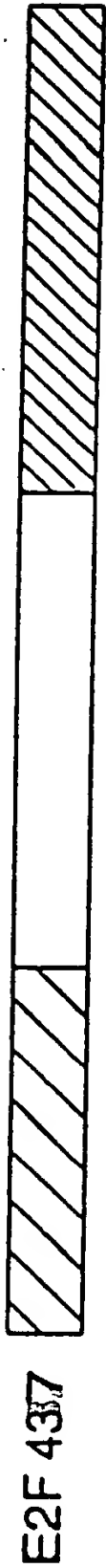


FIG. 9

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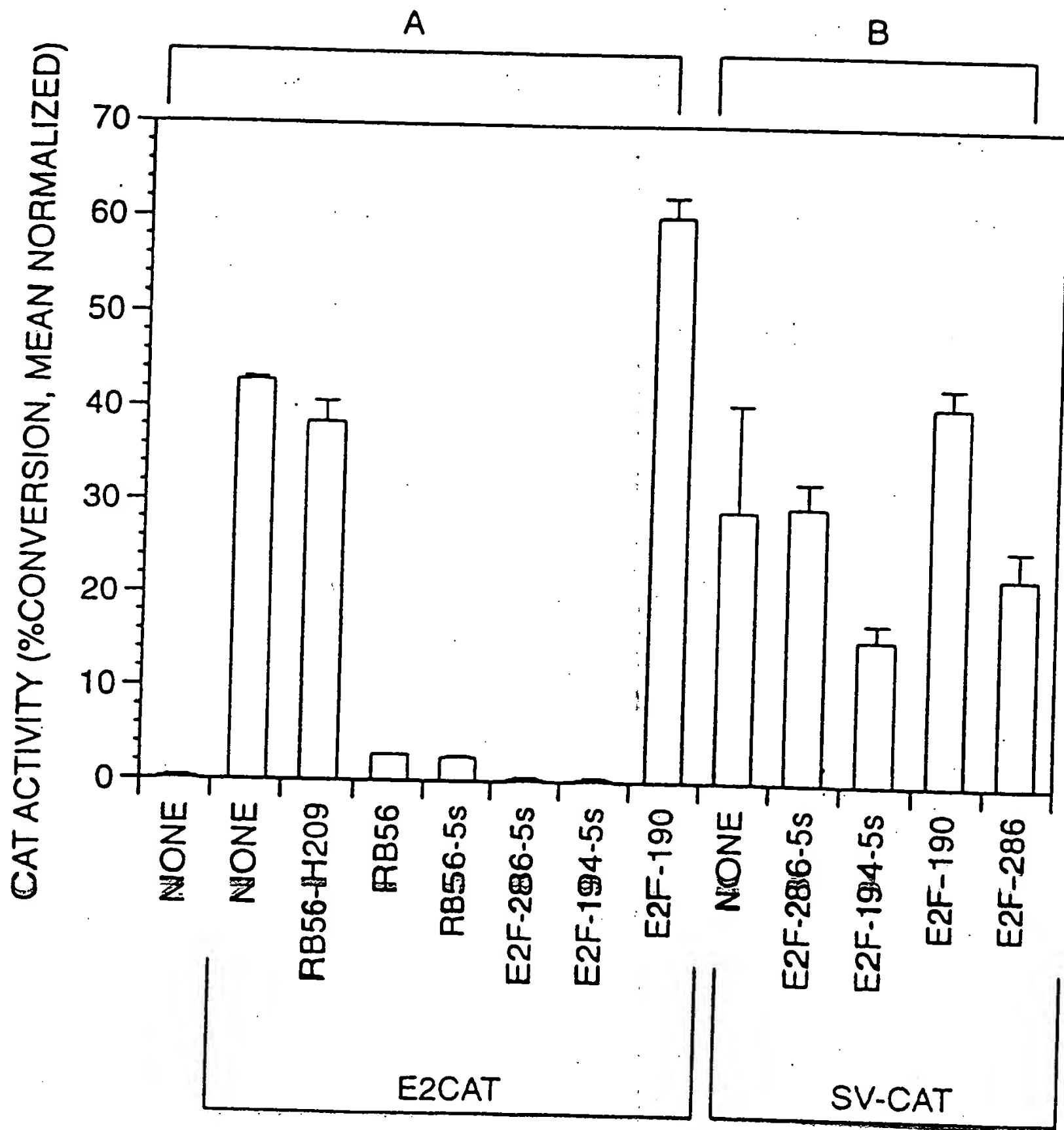


FIG. 10



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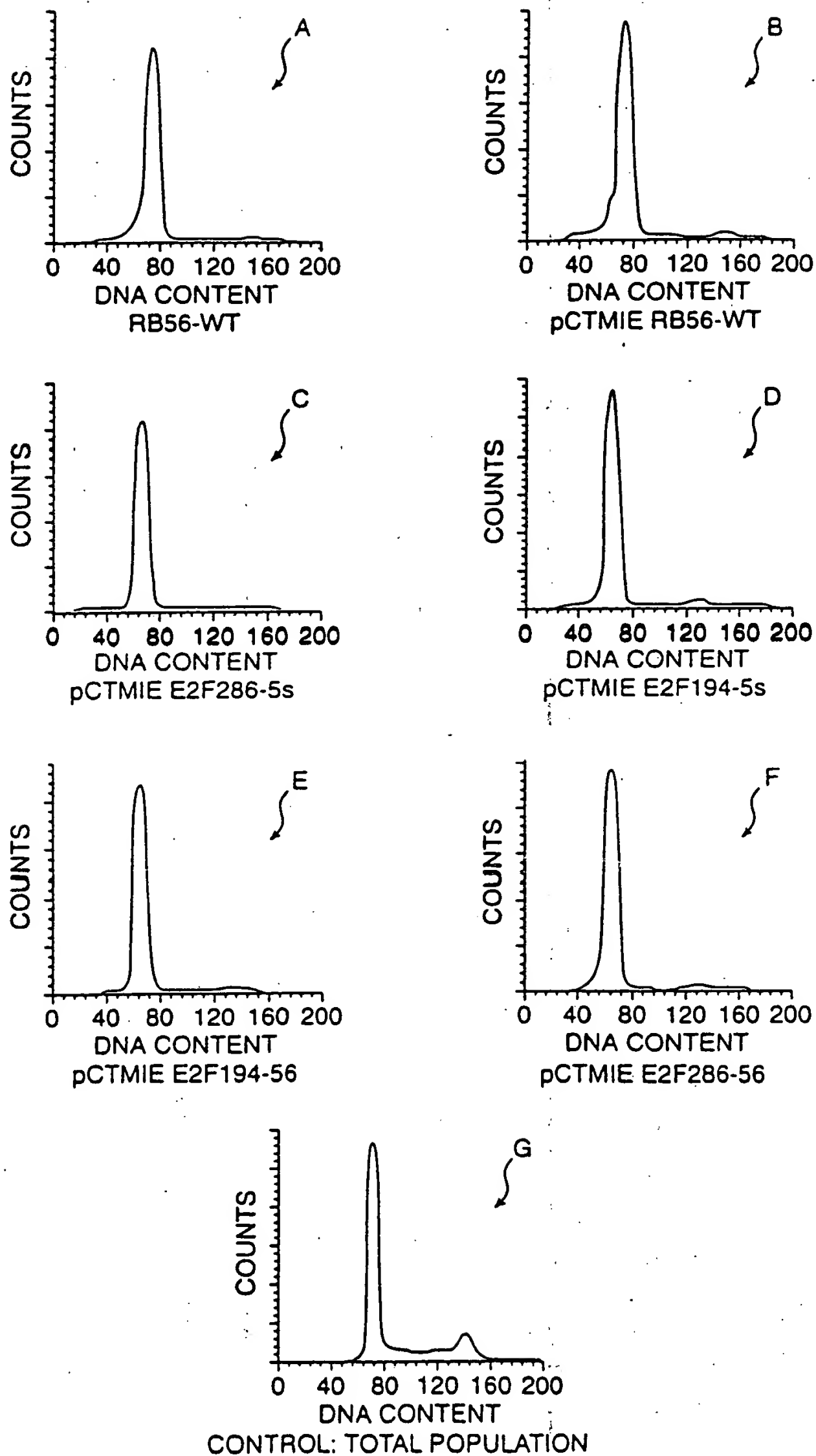


FIG. 12



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A7R5 (RAT SMOOTH MUSCLE)

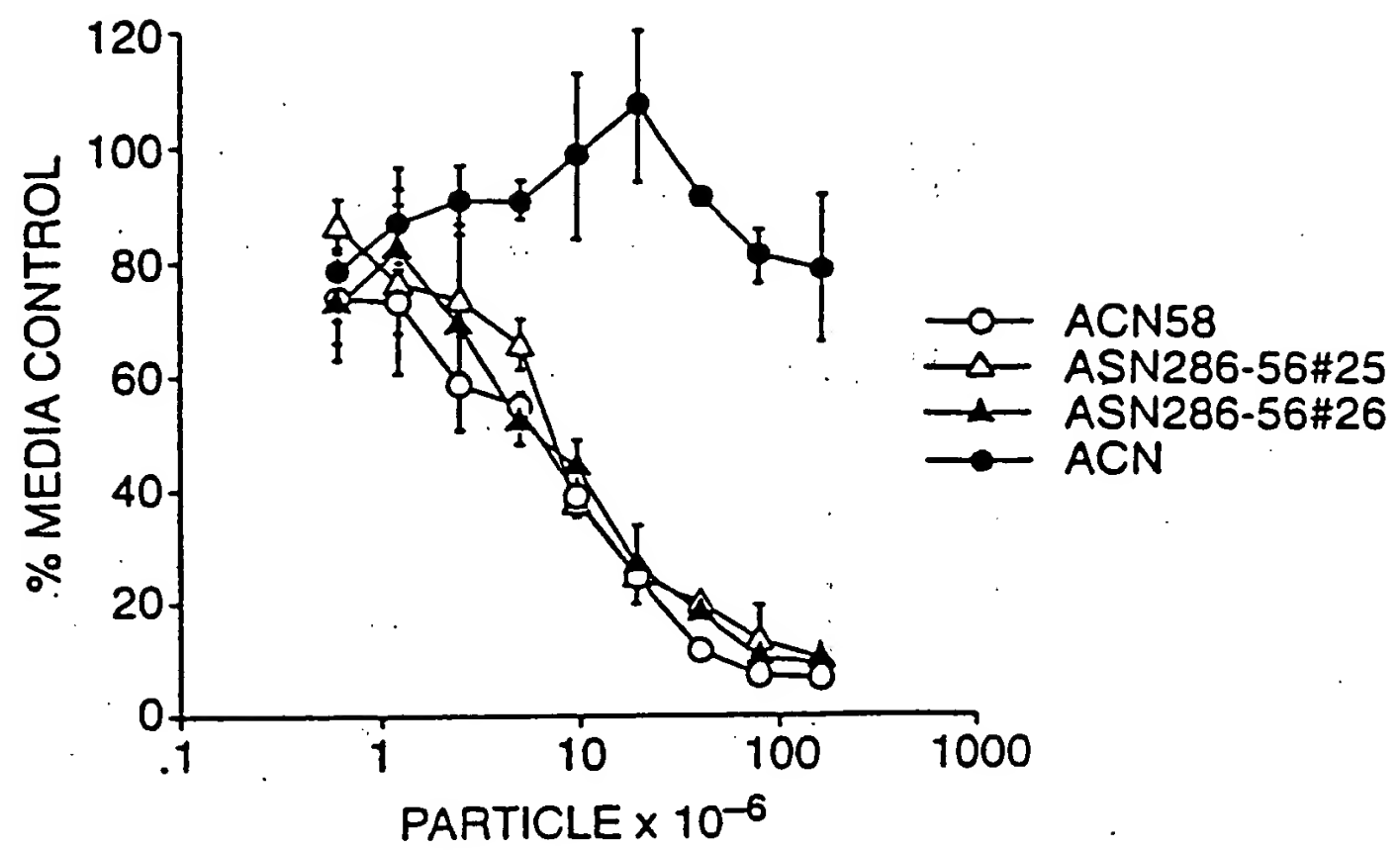


FIG. 13A

A10 (RAT SMOOTH MUSCLE)

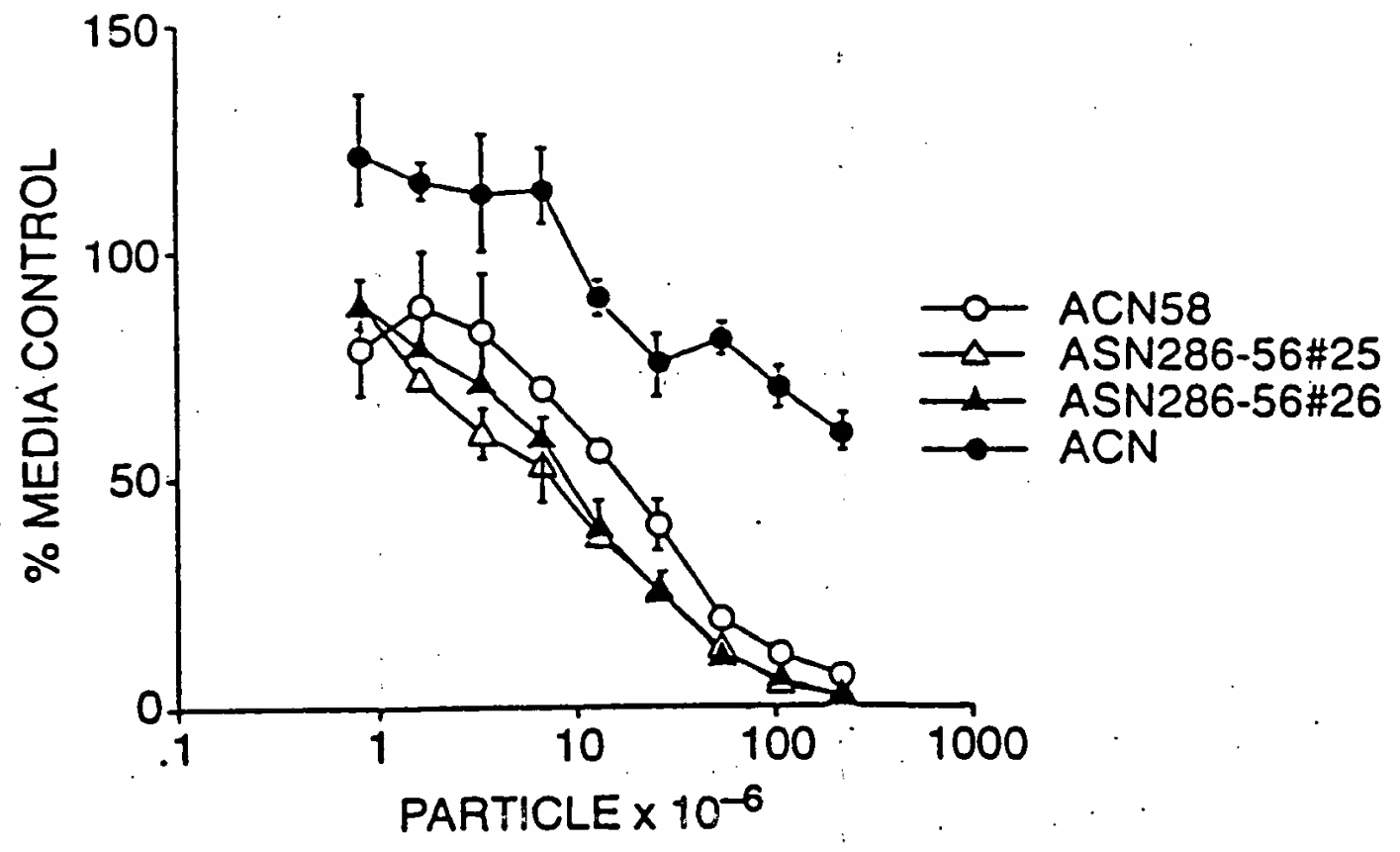


FIG. 13B



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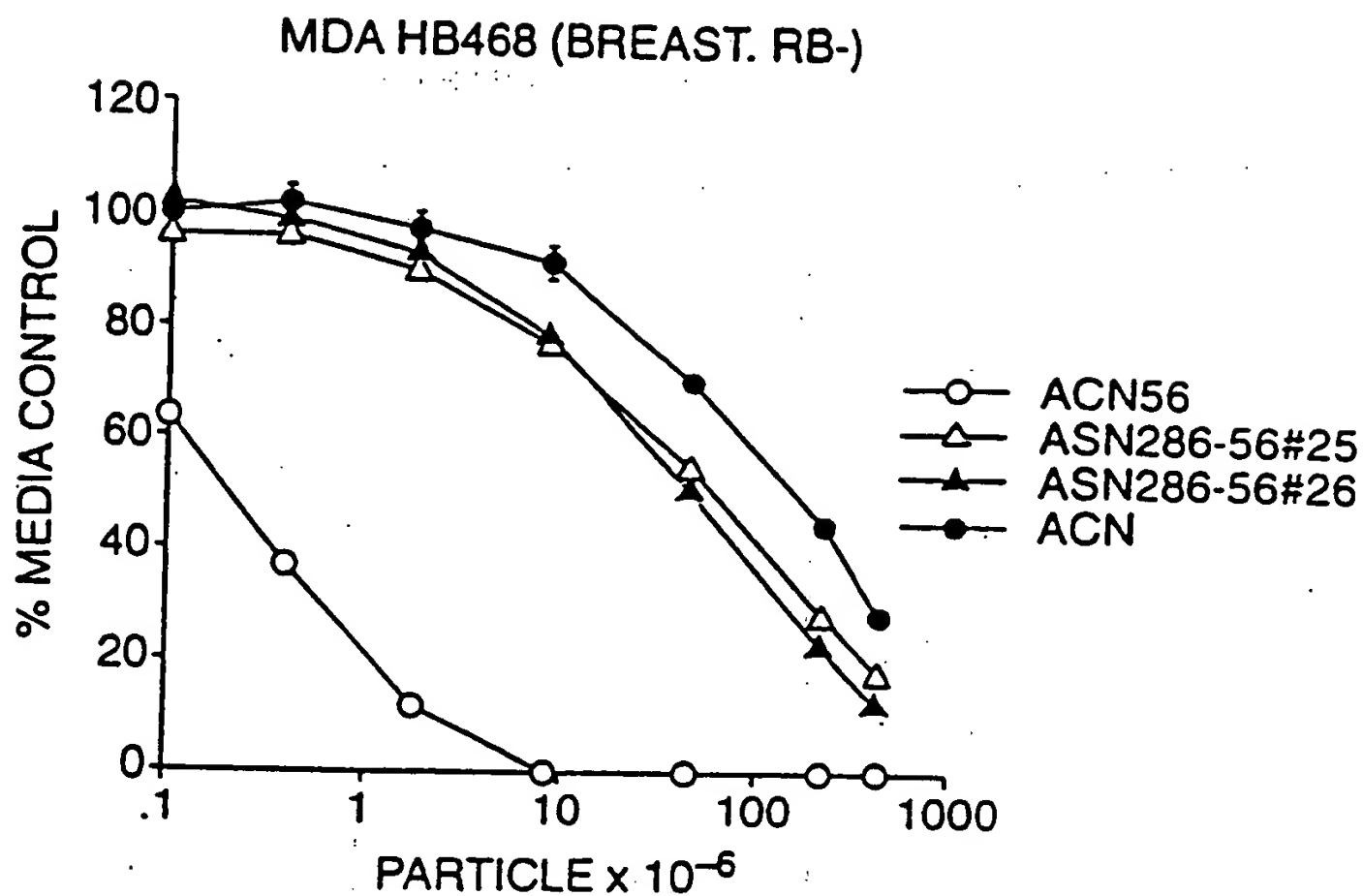


FIG. 14A

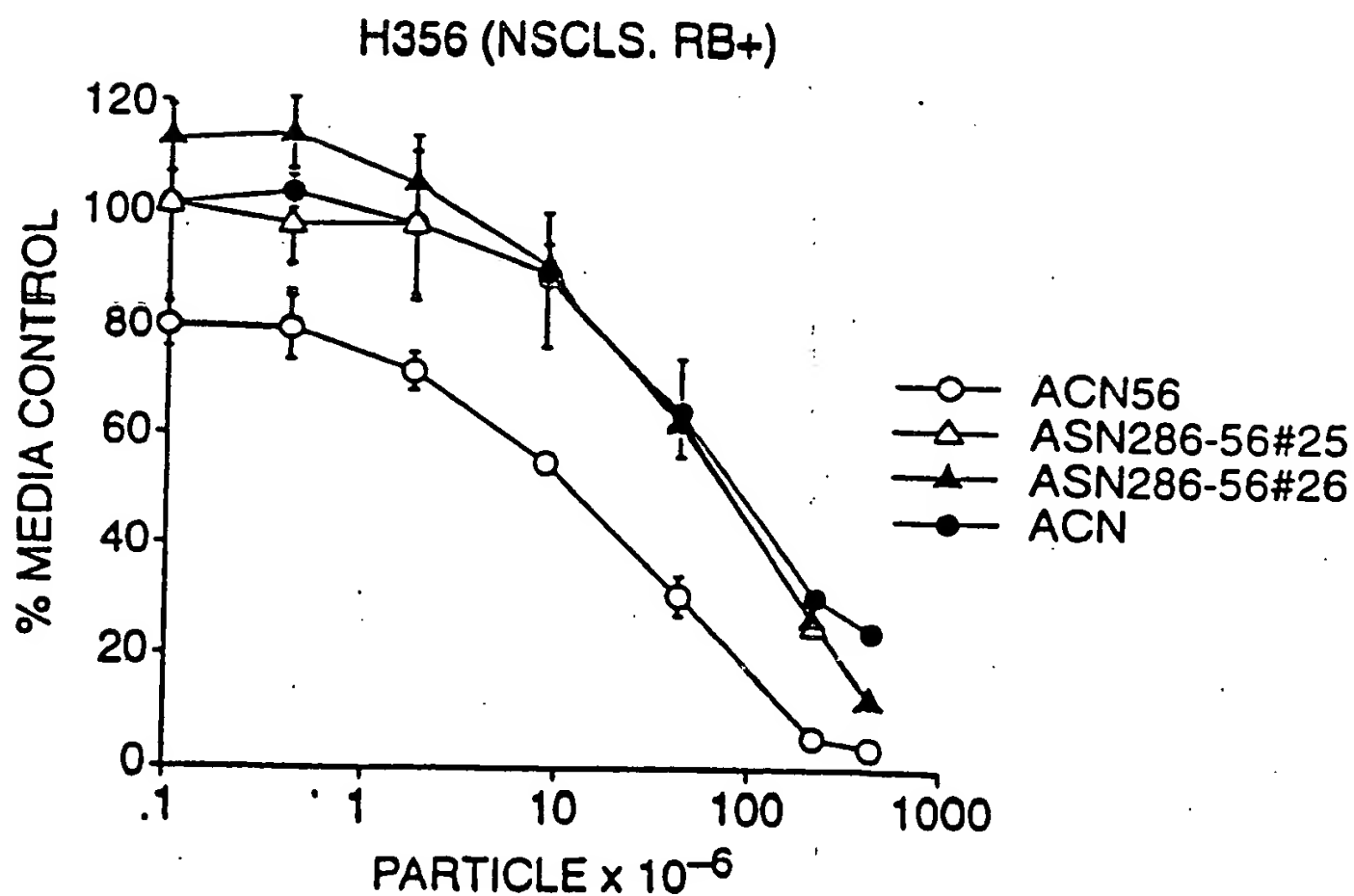
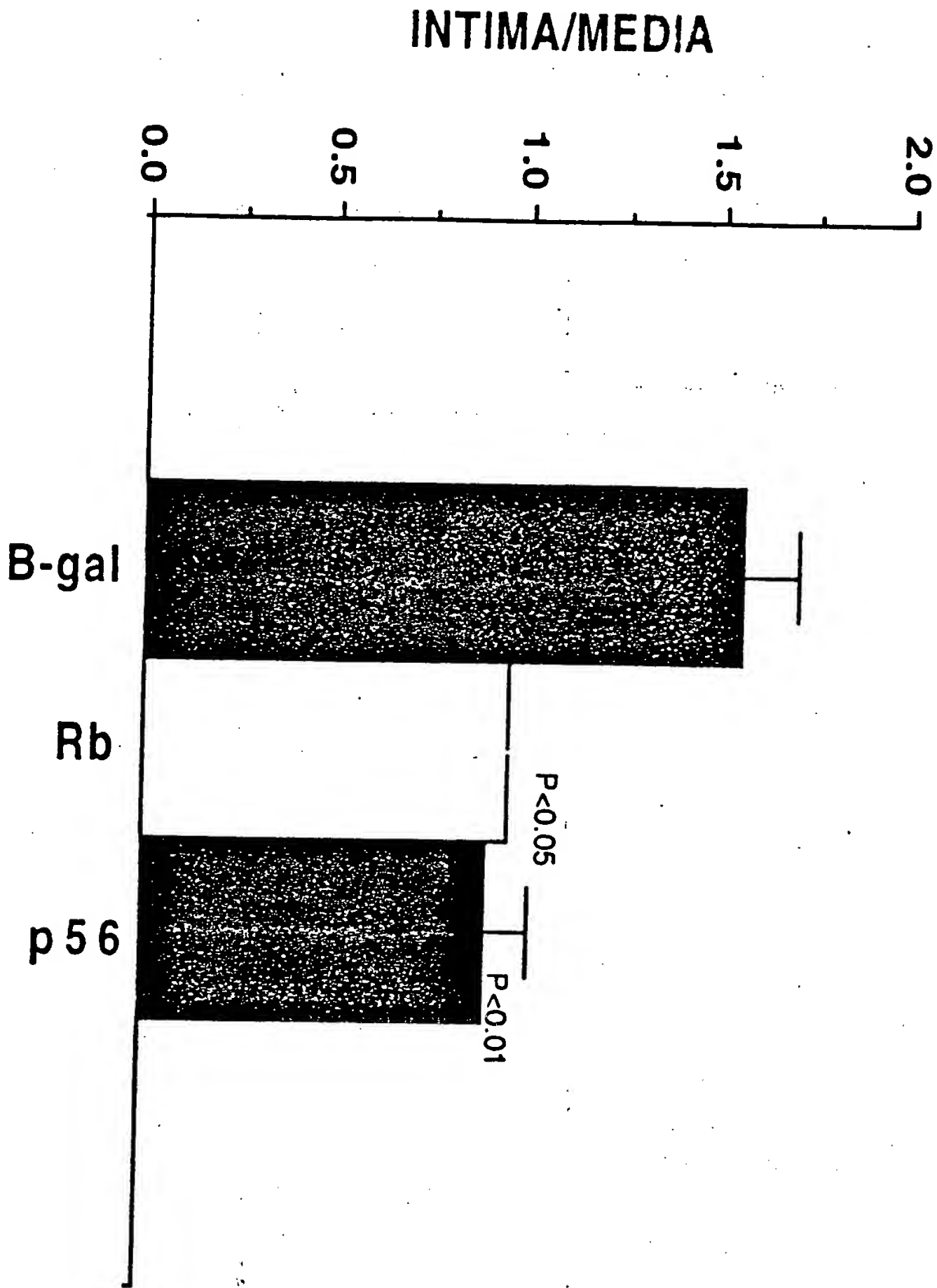


FIG. 14B



FIG. 17





A7r5 3H-THYMIDINE 83/83

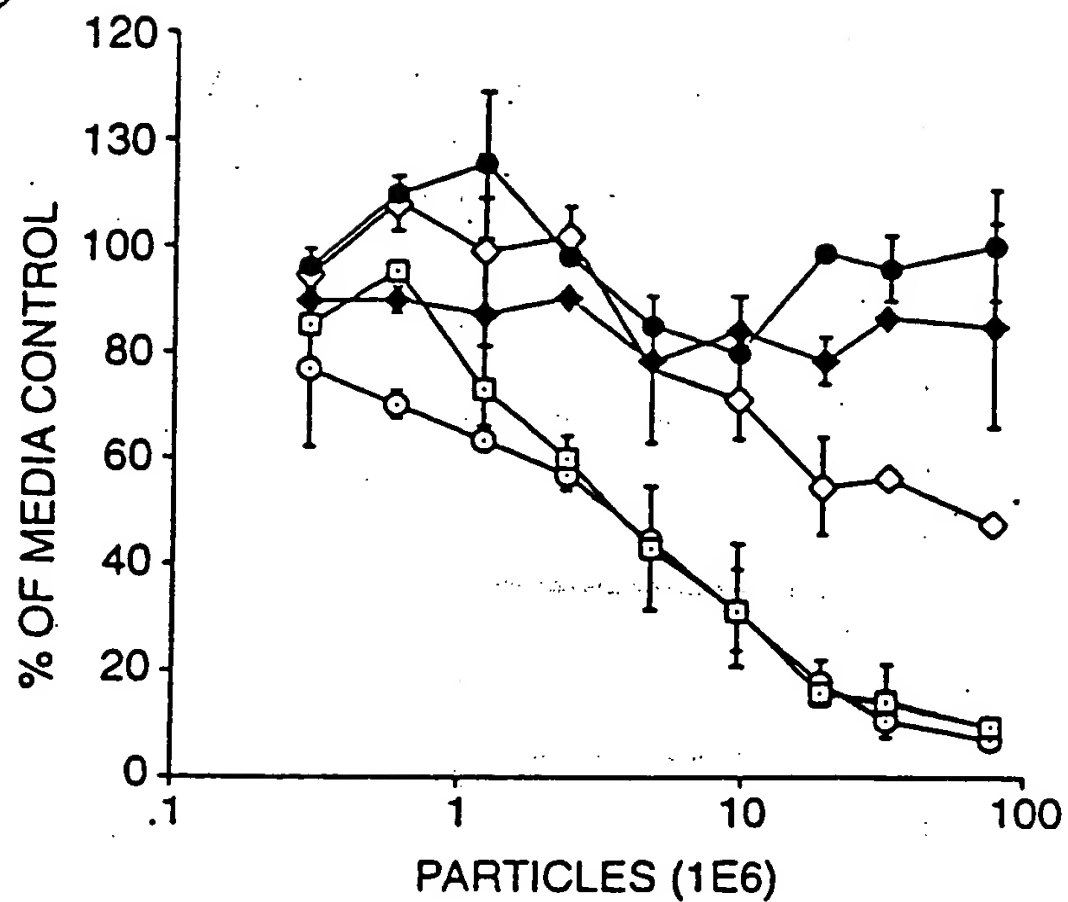


FIG. 21A

MDA468 3H-THYMIDINE

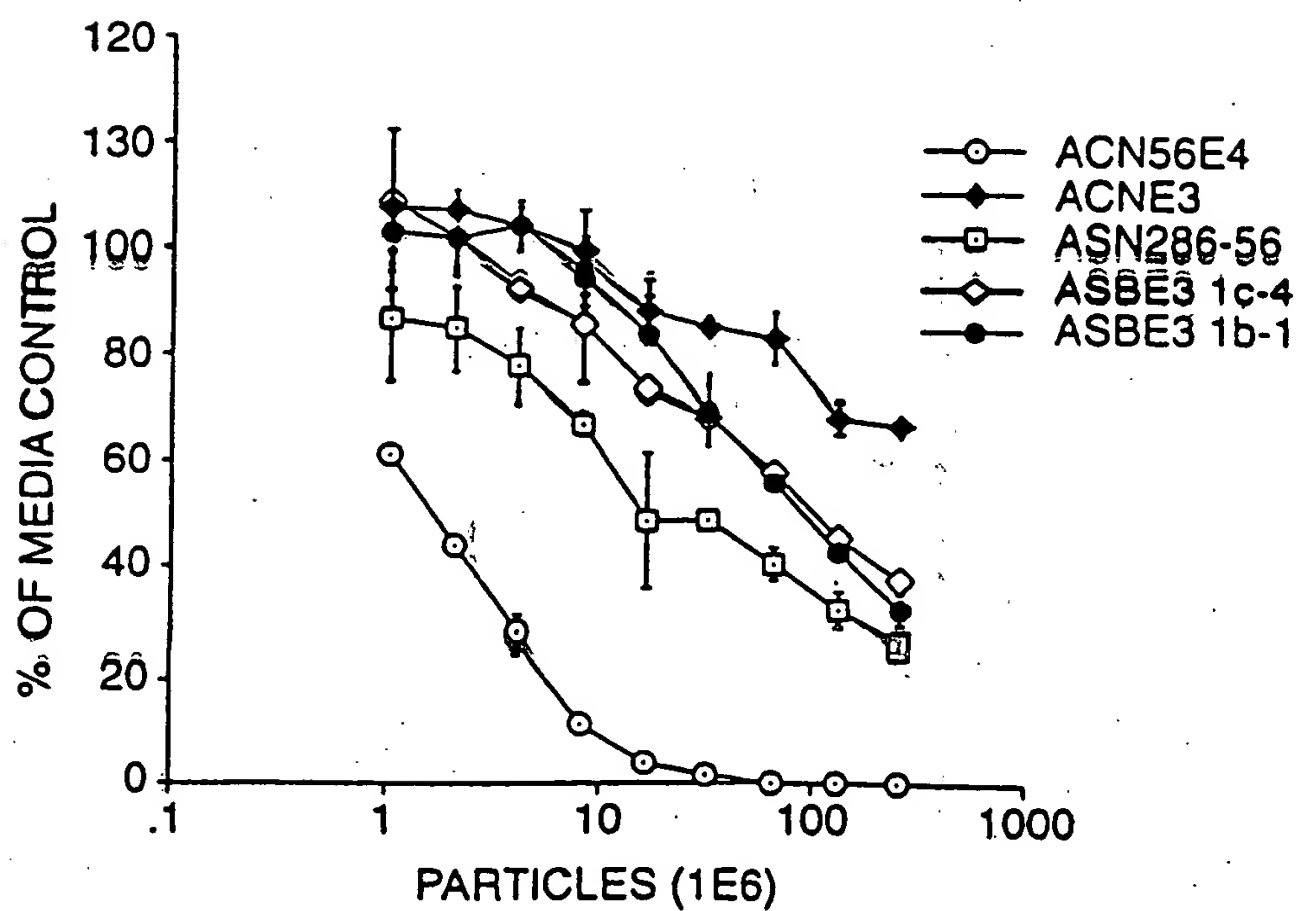


FIG. 21B



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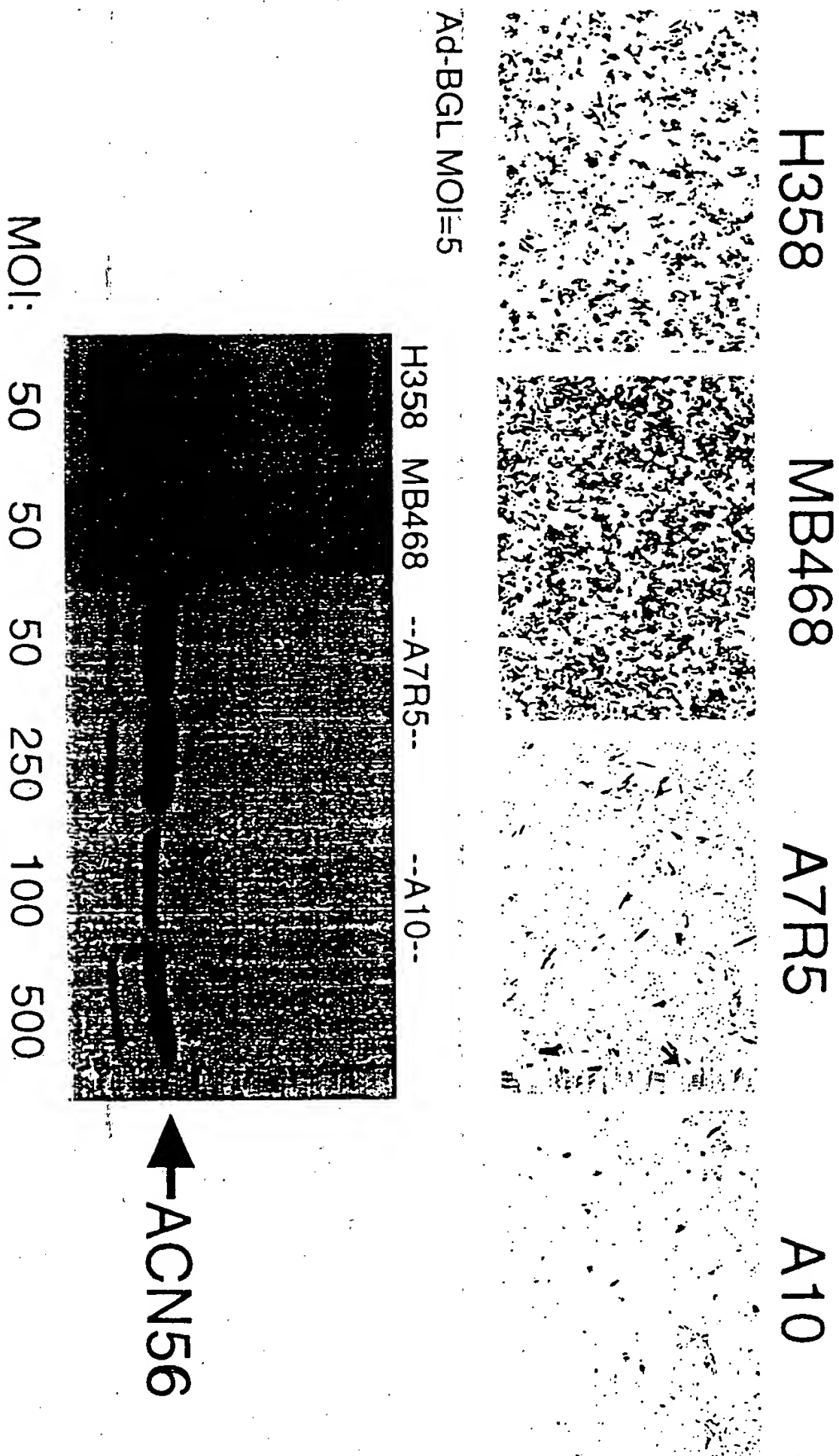


FIG. 15.



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FIG. 16.

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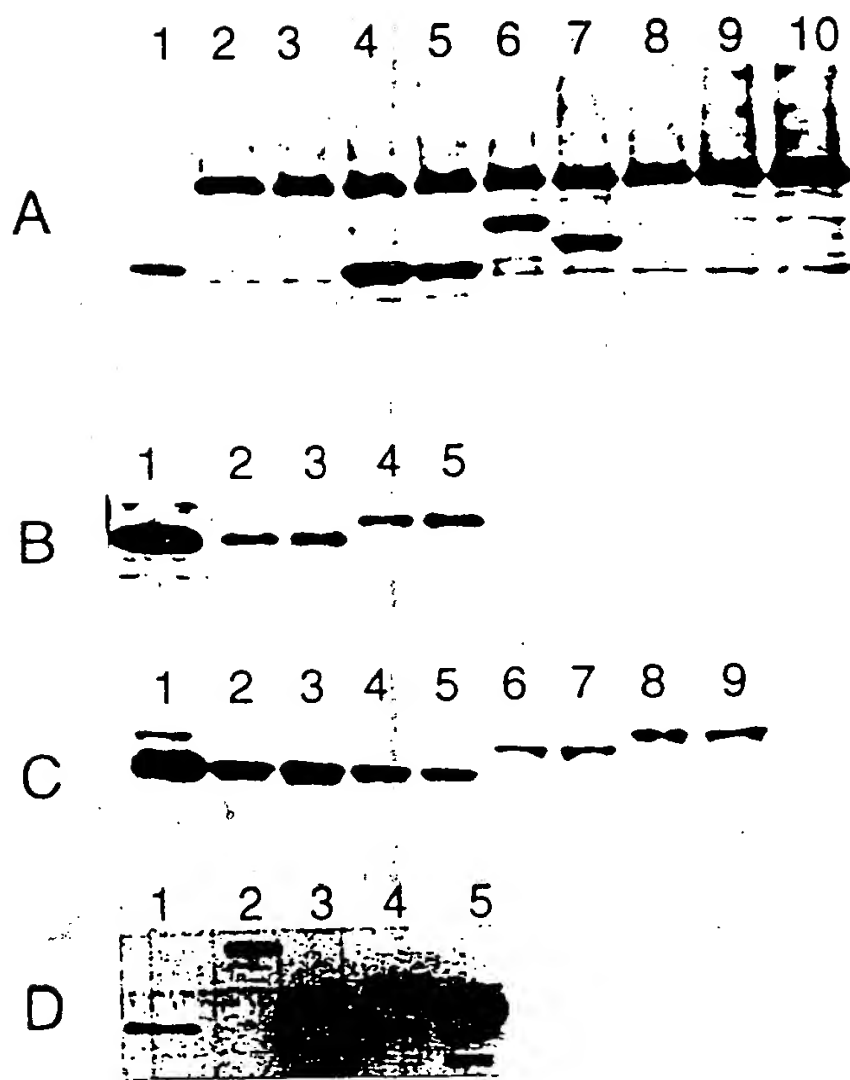


FIG. II.

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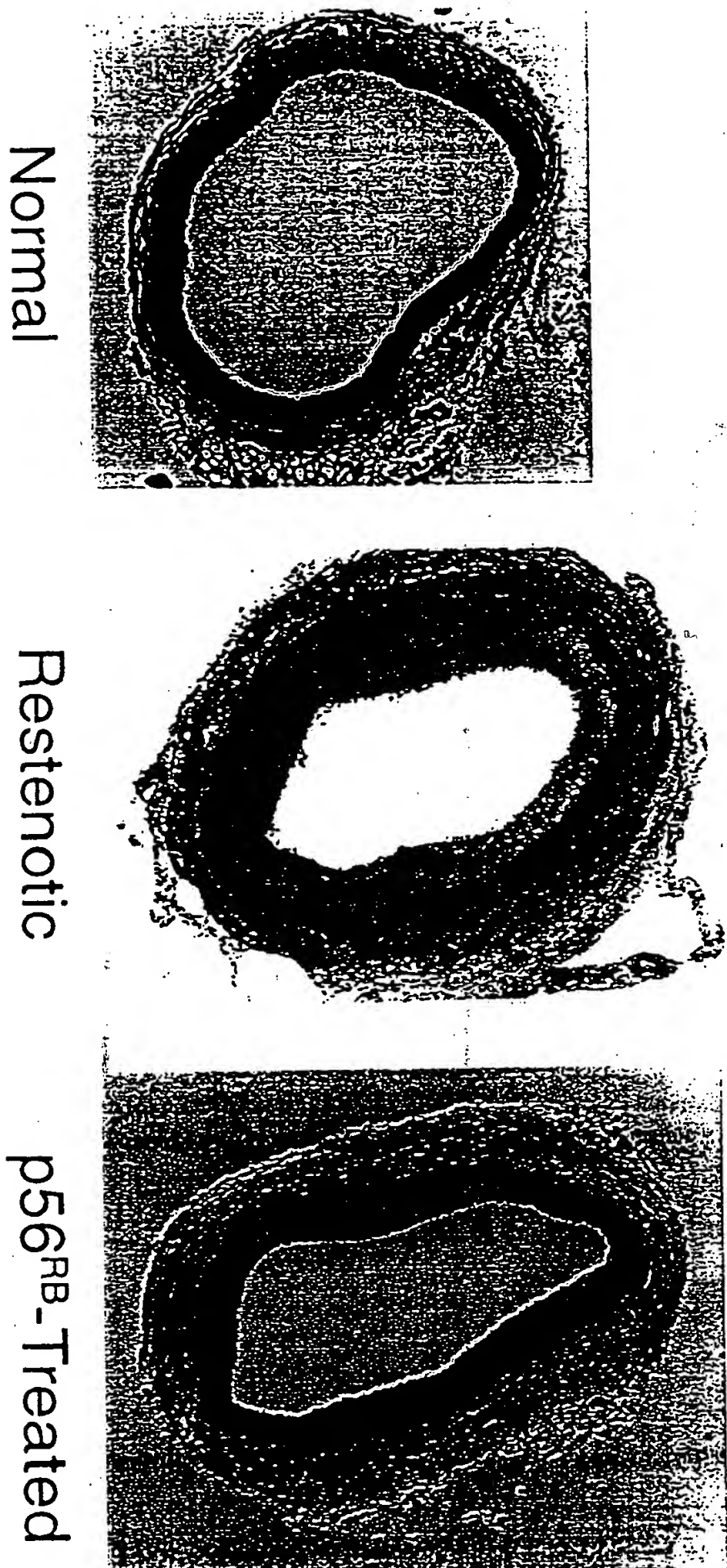


FIG. 18.

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MB468 (Breast)

MOI

A7R5 (Muscle)

ACNBGAL

1 1

ASNBGAL

100 50

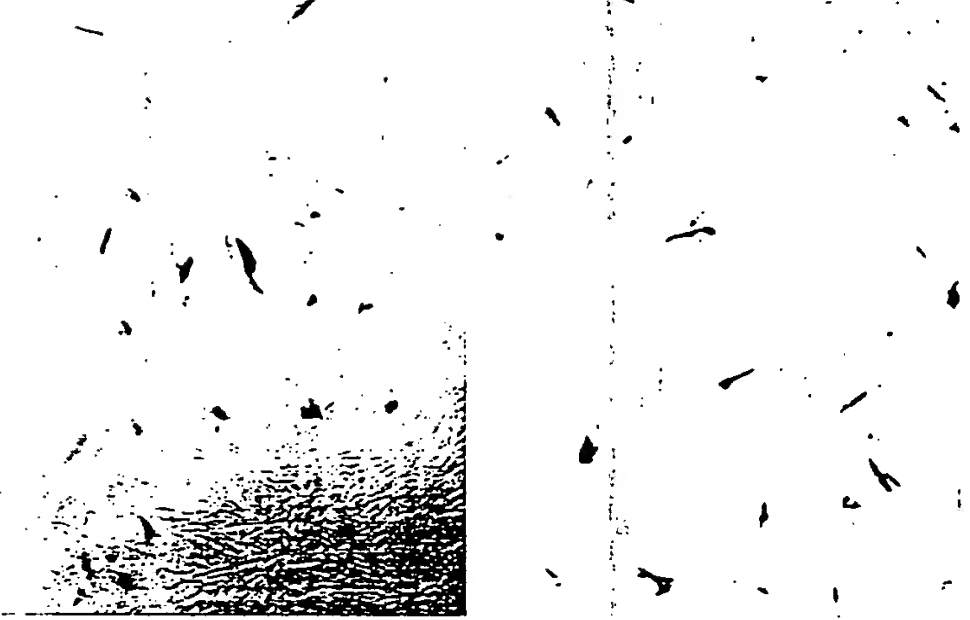


FIG. 19.

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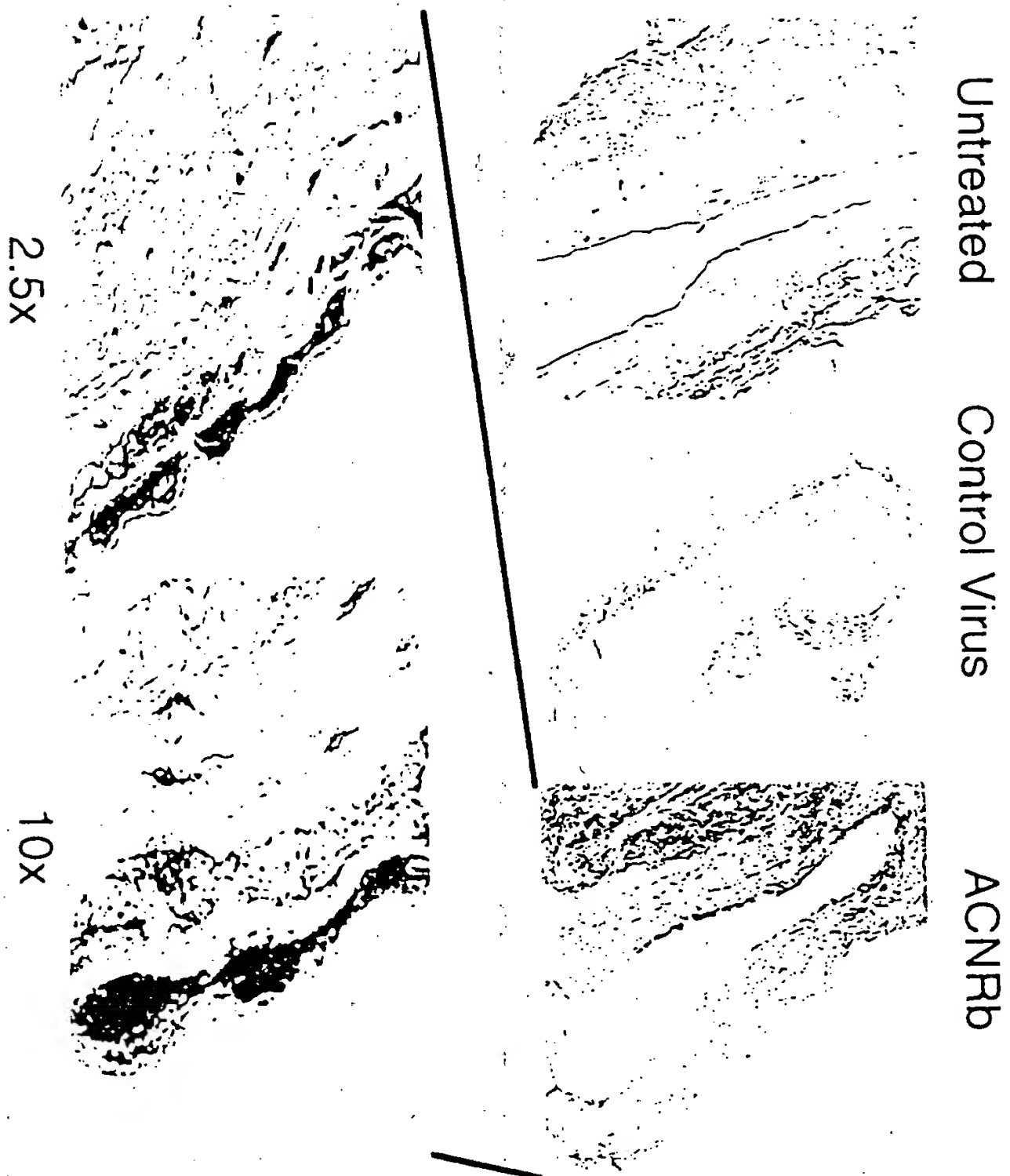


FIG. 20.

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